

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 07-24-02
Searcher: Beverly E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGN

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:10:30 ; Search time 2538.62 Seconds

(Without alignments)
1642.845 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309
Sequence: 1 atgcagataataagatga.....gggtatattgtccacacatag 309

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estt:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	228.6	74.0	332	9	AM619529 7594 MARC
C 2	183.8	59.5	731	9	AV398499 AV398499
C 3	140.4	45.4	240	9	AM659631 97104 MAR
C 4	139.8	45.2	785	9	AI547008 P42.1.13
C 5	123.8	40.1	223	10	C22108
C 6	117.2	37.9	160	10	BG895793 359430 MA
C 7	115.6	37.4	160	10	BG835172 359430 MA
C 8	109.4	35.4	336	10	BES21841 M22A1STM
C 9	106.2	34.4	162	10	BI338974 363710 MA
C 10	88.4	28.6	178	10	BI432815 EST55576
C 11	65.8	21.3	802	9	AI546999 P42.1.12
C 12	59.8	19.4	594	10	BE493915 WHE176_B
C 13	45.2	14.6	560	12	B84811 RPT11.128F7
C 14	45.2	14.6	634	12	AO309897 CITR1-EI-
C 15	42.8	13.9	532	9	AO544521 CITR1-EI-
C 16	42	13.6	299	12	AA547917 MB3D6V2G0
C 17	38.8	12.6	914	12	AZ539756 ENTG955TR

C 18	38.6	12.5	426	9	AV532310	AV532310
C 19	38.6	12.5	599	9	AV537481	AV537481
C 20	38.4	12.4	520	12	AZ927608	AZ927608
C 21	38	12.3	514	10	BM168198	BM168198
C 22	37.4	12.1	153	12	B88032	B88032
C 23	37.4	12.1	544	12	AZ525395	AZ525395
C 24	37.2	12.0	488	12	AG024048	AG024048
C 25	37.2	12.0	942	12	CNS02F0E	AL194459 Tetradon
C 26	37	12.0	404	10	BI514353	BI514353
C 27	37	12.0	458	10	BI510802	BI510802
C 28	37	12.0	559	10	BI510865	BI510865
C 29	36.8	11.9	478	9	AM288591	AM288591
C 30	36.8	11.9	582	12	AQ029690	AQ029690
C 31	36.8	11.9	646	12	AZ522631	AZ522631
C 32	36.8	11.9	681	10	BE658070	BE658070
C 33	36.4	11.8	733	10	BF680474	BF680474
C 34	36.2	11.7	500	9	AU086381	AU086381
C 35	36	11.7	617	12	AZ856405	AZ856405
C 36	36	11.7	713	12	BH029375	BH029375
C 37	36	11.7	1101	12	CNS01610	AL106770 Drosophila
C 38	35.8	11.6	494	10	BI745078	BI745078
C 39	35.8	11.6	496	9	AA842275	AA842275
C 40	35.6	11.5	885	12	CNS013ET	AL102767 Drosophila
C 41	35.4	11.5	771	9	AL516158	AL516158
C 42	35.4	11.5	1101	12	CNS05RM7	AL350728 Tetradon
C 43	35.2	11.4	392	10	BM258478	BM258478
C 44	35.2	11.4	468	9	AV618307	AV618307
C 45	35.2	11.4	581	9	AM573687	AM573687

ALIGNMENTS

RESULT 1
LOCUS AM619529/c
DEFINITION 7594 MARC PBE Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AM619529
VERSION AM619529.1 GI:7325713
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 332)
Smith,T.P.L., Fahrenkrug,S.C., Rohrer,G.A., Simmen,F.A., Rexroad
C.E. and Keefe,J.W.
Mapping of expressed sequence tags from a porcine early embryonic
CDNA library
Anim. Genet. 32 (2), 66-72 (2001).
21314990
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases cycled and alt. trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 18
and -match 12 options.
PCR Primers
FORWARD: GGAAACGCTATGACCATG
REVERSE: GTAAACGACGCGCAGT
BACKWARD: GGAAACGCTATGACCATG
Seq primer: AATTACCCCTAATAAGG.
Location/Qualifiers
1..332
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC PBE"
/issue_type="day 12 whole embryos"
/lab_host="XOLR"
/note="Vector: pBLUESCRIPT SK-; Site_1: EcoRI; Site_2:
XhoI; Library made from pool of embryos in spherical and

75 TTTTGGGGCCGAGAAAATGTTGTTAAACAGAAACCCGCAAAATTCCTCCANANAGAT 16
 100 CCGCGCGGCGAGAAAACGTCGCAAAAACCGAGCAAAAACCGCAAAAACCGCAAAAAC 244
 271 CCGCGCGGCGAGAAAACGTCGCAAAAACCGAGCAAAAACCGCAAAAACCGCAAAAAC 244

ACCESSION	BG895793
VERSION	BG895793.1
	GI:14

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VERSION      00000000
KEYWORDS     BG895793.1  GI:14306034
EST          1
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SOURCE pig.
ORGANISM Sus scrofa
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 160)
AUTHORS Fahrrentug,S.C., Frickling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.M., and Keeler,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 123 row: L column: 23
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_11b="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT 46 a 37 c 31 g 46 t
ORIGIN
Query Match 37.9%; Score 117.2; DB 10; Length 160;
Best Local Similarity 93.8%; Pred. No. 7.1e-22;
Matches 122; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 179 ccaaaattgttgctgagaaatgtgttaaaacagaactcagcaaatcgttaa 238
160 ccaaaattgttgctgagaaatgtgttaaaacagaactcagcaaatcgttaa 101
DB 239 atgagattgctggtttatcactcttgcatctatactcgcgtggaagccgggtatatt 298
100 atgagattgctggtttatcactcttgcatctatactcgcgtggaagccgggtatatt 41
QY 299 gctcacata 308
40 gctcacata 31
DB 40 gctcacata 31

RESULT 7
LOCUS BG835172/c 160 bp mRNA linear EST 25-MAY-2001
DEFINITION BG835172 353618 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG835172.1 GI:14201080
VERSION BG835172.1
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE -1 (bases 1 to 160)
AUTHORS Fahrrentug,S.C., Frickling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.M., and Keeler,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

JOURNAL Unpublished (2000)
COMMENT Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 116 row: L column: 23
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_11b="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT 47 a 37 c 31 g 45 t
ORIGIN
Query Match 37.4%; Score 115.6; DB 10; Length 160;
Best Local Similarity 93.1%; Pred. No. 1.9e-21;
Matches 121; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 179 ccaaaattgttgctgagaaatgtgttaaaacagaactcagcaaatcgttaa 238
160 ccaaaattgttgctgagaaatgtgttaaaacagaactcagcaaatcgttaa 101
DB 239 atgagattgctggtttatcactcttgcatctatactcgcgtggaagccgggtatatt 298
100 atgagattgctggtttatcactcttgcatctatactcgcgtggaagccgggtatatt 41
QY 299 gctcacata 308
40 gctcacata 31
DB 40 gctcacata 31

RESULT 8
LOCUS BE521841 336 bp mRNA linear EST 19-MAR-2001
DEFINITION M22A1STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M22A1 5', mRNA sequence.
ACCESSION BE521841
VERSION BE521841.1 GI:9779819
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 336)
AUTHORS White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Iarduya,O., Jaworski,J.G., Ohlrogge,J., and Banning,C.
TITLE A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
COMMENT Contact: Banning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
USA
Tel: 517 355 1609
Fax: 517 353 9334

/organism="Sus scrofa"

his sequence is actually derived from *Phytophthora infestans* than potato."

RESULT 12

RESULT 13

LOCUS	560 bp	DNA	linear	GSS 09-APR-1999
B84811				
DEFINITION	RPrC11-28F7..np RPrC1-11 Homo sapiens genomic clone RPrC1-11-28F7, DNA			
ACCESSION	sequence.			
B84811				

VERSION	B84811.1	GI:2925943
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 560)	
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.K., Golden,K., Berry,K., Granger,D., Sun,E., Wible,C., de Jong,P. and Venter,J.C.	
TITLE	Use of BAC End Sequences for Sequence-Ready Map Building (1998)	
JOURNAL	Unpublished (1998)	
COMMENT	Other GSSs: RPC11-28F7.TV Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: maddams@tigr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Piter de Jong (piter@jng.med.buffalo.edu). Clones may be purchased from BACPac Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (inforesgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/Bac_end_search.html Seq primer: SP6 Class: BAC ends.	
FEATURES	Location/Qualifiers	
SOURCE	1..560	
	/organism="Homo sapiens"	
	/db_xref="GDB:751049"	
	/db_xref="taxon:9606"	
	/clone="RPC1-11-28F7"	
	/clone_11b="RPC1-11"	
	/sex="Male"	
	/cell_type="lymphocytes"	
	/note="vector: pBACes.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC Library"	
BASE COUNT	240 a 106 c 82 g 132 t	
ORIGIN		
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	Best Local Similarity 48.8%; Pred. No. 0.049;	
	Matches 122; Conservative 0; Mismatches 128; Indels 0; Gaps 0;	
OY	8 ataataagatgaaaaaatgtattattttctgcgcgcctcggcaatgcttatlacaggatgtg 67	
Db		
	269 ATTAAACAAGCAAGGATGCTTACTTTTGTCATGCCCATCCAMATATACTATTAGAAGTG 328	
OY	68 ctcaacaacgcttactcttcttggaacaacaacgacagcacagtaccaccaagaagaccatca 127	
Db		
	339 CTAGCCAGAACACATAGGTAGATTAATCAAAAGGGCTCAAAAACAAAAAAGAAAGTCAANA 388	
OY	128 ctcatcattcttcgttcgcggaattggacaagaagaacctgtgatcgacgccaaatlt 187	
Db		
	389 TATCTCTCATCATGTGATTATAAATTTCTATACTATAGAACCTCGAGACACCACCAANA 448	
OY	188 gtggcgggtgcagaaaatttgtttaaacagaacacgcagcaaacatctcgtaattgattgc 247	
Db		
	449 CTCCTGGACACGATATATGTCAGTAAAGTTTCAGATACAAATTAAGTGCACAAAATATMG 508	
OY	248 tcggtttat 257	
Db		
	509 TAGCATTTTYT 518	
RESULT 14		
LOCUS	AO309897 634 bp DNA linear GSS 22-DEC-1998	
DEFINITION	CITR1-EI-2522C23.TR CITR1-EI Homo sapiens genomic clone 2522C23, DNA sequence.	

ACCESSION	A0309897
VERSION	A0309897.1
KEYWORDS	GSS.
SOURCE	GI:4041784
ORGANISM	human.
TITLE	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 634)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linber,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
JOURNAL	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1998) Other_GSSs: CITBI-EI-2522C23.TF
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13 Reverse Class: BAC ends.
FEATURES	Location/Qualifiers 1..634 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2522C23" /clone_1lb="CITBI-EI" /sex="male" /cell_type="sperm" /note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"
BASE COUNT	274 a 123 c 89 g 148 t
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Best Local Similarity	48.8%; Pred. No. 0.05; Matches 128; Indels 0; Gaps 0;
Matches 122; Conservative	0; Mismatches 128; Indels 0; Gaps 0;
Oy	8 ataatgaagatgaaaaaaatgtattcttcgcgcctcgcaatgctttatcagatgtg 67
Dd	309 ATTAAACAAGCAAGATGCTTACTTTTGCTACTCCCATCCAAOATGTACTAAGTg 368
Oy	68 ctcaacaacglttactgttgyaaaacaaccgcagcagtaacacccaagaagaaacctca 127
Dd	369 CTAGCCAAACAACTACAGTAAGATAATCAACAAAGGGGTCAAAAAGAAAGTCAAAA 428-
Oy	128 ctcatcattcttgcttcgcggaaattgagcaagaagaaacgtgtgatcgagccaaattt 187
Dd	429 TATCTCTCATCATGTGATTATATAAATTCTATACTAGAGAACCCTGGAGACACCACCAAAGA 488
Oy	188 gtgagggtgcgaanaattgtttaaacagaacaccgcgaacacatctgtaagtattgac 247
Dd	489 CTCCTGGTAGCATATATGTCAGTAAAGTTTCAGGATACCAATAATGAAGTACAAAAATTAG 548
Oy	248 tcgatttat 257
Dd	549 TAGCATTTTT 558
RESULT	15
LOCUS	A0544521
DEFINITION	CITBI-EI-2636G14.TR CITBI-EI Homo sapiens genomic clone 2636G14,
ACCESSION	A0544521
VERSION	A0544521.1 GI:4904043

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 532)

AUTHORS

Zhao, S., Adams, M.D., Nierman, W., Majek, J., Shizuya, H., Simon, M. and Venter, J.C.

TITLE

Use of BAC End Sequences from Caltech Libraries for Sequence-Ready

JOURNAL

Map Building

COMMENT

Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet1gr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..532
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2636G14"
/clone_lib="CIBR-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT

225 a 102 c 80 g 125 t

ORIGIN

Query Match 13.9%; Score 42.8; DB 12; Length 532;
Best Local Similarity 50.5%; Pred. No. 0.22;
Matches 104; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

OY 8 ataataagatgaaaaaatgtattttctgcgcgtctgcgaatgcttattacagatgtg 67
DB 310 ATTAGAACAAAGACAGATGCTTCTTGTCTCTCCATCCCAACATAGTACGAGTG 369
Y 68 ctcaacaacagcttactgtgtgaaacacgacagcagtaacacccaaggaaacatca 127
DB 370 CTAGCCAGAACATAGTAAATCAAAAGCGTCAAAACATATAAGAAAGTCATAA 429
OY 128 cctcatcttcttcgttcggaattgacaagagaagaactgtgtgacgccaattt 187
DB 430 TATCTCTCATCATGATTATAAATCTTACTAGAGAACCTGAGACACACCAAGA 489
OY 188 gtggcggtgcagaaaatgtttaa 213
DB 490 CTCCTGTACTGATATGTCAGTAAA 515

Search completed: July 23, 2002, 13:10:31
Job time: 7537 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:45:07 ; Search time 99.46 Seconds
(without alignments)
763.128 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309
Sequence: 1 atcagagataataagatgaa.....gggtatattgctcacaatag 309

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
4: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
5: /cgn2_6/prodata/2/lna/PCRTUS_COMB.seq:*
6: /cgn2_6/prodata/2/lna/Backfilist1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length DB	ID	Description
1	309	100.0	309	3	US-09-023-221A-22	Sequence 22, Appl
2	309	100.0	309	4	US-09-282-352A-22	Sequence 21, Appl
3	309	100.0	378	4	US-09-023-221A-21	Sequence 21, Appl
4	309	100.0	378	4	US-09-282-352A-21	Sequence 1, Appl
5	309	100.0	760	3	US-09-023-221A-1	Sequence 1, Appl
6	309	100.0	760	4	US-09-282-352A-1	Sequence 1, Appl
7	273.2	88.4	309	3	US-09-023-221A-5	Sequence 5, Appl
8	273.2	88.4	309	4	US-09-282-352A-5	Sequence 5, Appl
9	252	81.6	309	3	US-09-023-221A-6	Sequence 6, Appl
10	252	81.6	309	4	US-09-282-352A-6	Sequence 6, Appl
11	252	81.6	11933	4	US-09-470-618-13	Sequence 13, Appl
12	252	81.6	11933	4	US-09-364-862-13	Sequence 13, Appl
13	34.2	11.1	1519	4	US-09-002-361-4	Sequence 4, Appl
14	33.6	10.9	1817	2	US-08-743-637B-1	Sequence 1, Appl
15	33.6	10.9	1817	3	US-08-526-840B-1	Sequence 1, Appl
16	32.8	10.6	4380	1	US-07-582-941-1	Sequence 1, Appl
17	32.8	10.6	4380	2	US-08-453-141-1	Sequence 1, Appl
18	32.8	10.6	4380	3	US-08-453-141-1	Sequence 1, Appl
19	32.4	10.5	1925	3	US-08-553-436A-1	Sequence 1, Appl
20	32.2	10.4	408	4	US-09-328-111-169	Sequence 169, App
21	32.2	10.4	1690	1	US-08-276-452A-24	Sequence 24, Appl
22	32.2	10.4	1690	2	US-08-798-744-24	Sequence 24, Appl
23	31.2	10.1	90050	4	US-09-245-041-5	Sequence 5, Appl
24	30.6	9.9	1504	4	US-08-878-989-10	Sequence 10, Appl
25	30.6	9.9	1504	2	US-09-272-796-10	Sequence 1, Appl
26	30.6	9.8	1576	4	US-09-197-378-1	Sequence 1, Appl
27	30.2	9.8	2089	1	US-08-552-142A-1	Sequence 1, Appl

C 28	30.2	9.8	2089	1	US-08-910-973-1	Sequence 1, Appl
C 29	30.2	9.8	2089	5	PCT-US95-05741-1	Sequence 1, Appl
C 30	29.8	9.6	2431	3	US-08-714-918-15	Sequence 15, Appl
C 31	29.8	9.6	2431	4	US-09-265-315-15	Sequence 15, Appl
C 32	29.8	9.6	2431	4	US-09-265-315-15	Sequence 15, Appl
C 33	29.8	9.6	2431	4	US-09-266-417-15	Sequence 15, Appl
C 34	29.8	9.6	2431	4	US-08-788-892-1	Sequence 1, Appl
C 35	29.6	9.6	2525	3	US-08-714-918-84	Sequence 84, Appl
C 36	29.6	9.6	2525	4	US-09-265-315-84	Sequence 84, Appl
C 37	29.6	9.6	2525	4	US-09-265-315-84	Sequence 84, Appl
C 38	29.6	9.6	2525	4	US-09-265-315-84	Sequence 84, Appl
C 39	29.6	9.6	3825	3	US-08-904-263A-3	Sequence 3, Appl
C 40	29.4	9.5	237	3	US-08-904-263A-3	Sequence 3, Appl
C 41	29.4	9.5	846	2	US-08-743-637B-189	Sequence 189, App
C 42	29.2	9.4	595	4	US-09-385-982-25	Sequence 25, Appl
C 43	28.8	9.3	906	2	US-08-951-871-5	Sequence 5, Appl
C 44	28.8	9.3	4248	3	US-08-678-614-1	Sequence 1, Appl
C 45	28.6	9.3	3414	1	US-07-973-320-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-023-221A-22
Sequence 22, Application US/09023221A
Patent No. 6087128
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-22

Query Match 100.0%; Score 309; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.4e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 atcagagataataagatgaaatgttttttcgcgcctctggcaatcattattaca 60
|||||
1 atcagagataataagatgaaatgttttttttcgcgcctctggcaatcattattaca 60

QY 61 ggaatgctcaacaacggttactgttggaaacaacccgacagagtaacacccaaggaa 120
DB 61 GGATGCTCAACAACGTTACTGTGGAACAACCGACAGCATACCAAGAA 120
QY 121 accatcctcattcttcttctgttcgggaattggacaagaaacgttgatgcagcc 180
DB 121 ACCATCCTCATCTTCTTCTGTTCGGGAATGGACAAGAAACGTTGATGCAGCC 180
QY 181 aaattgtgagcggtgcagaaatgttcttaaacagaaactcagcaacattcgtaaat 240
DB 181 AAATTTGTGGCGGTGCAGAAATGTGTAAAAACAGAACTCAGCAAACTTCGTAAT 240
QY 241 ggaatgctcggtttatcacttcttgatcactatcccgctggaagccgggtatattgc 300
DB 241 GGATGCTCGGTTTATCATCTTTGCGATCTATCTCGCTGGAAGCCGGGTATATTGC 300
QY 301 tcacaatag 309
DB 301 TCACAATAG 309

RESULT 2

US-09-282-352A-22
Sequence 22, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-282-352A-22

Query Match 100.0%; Score 309; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5,4e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgagagataataagatgaaataatgtttttctgcgcgtctggaagatcattataca 60
DB 1 atgagagataataagatgaaataatgtttttctgcgcgtctggaagatcattataca 60

DB 1 ATGCAGGTAATAAGATGAAAAAATGTTATTTCTGCCGCTCGCAATGCTTATTACA 60
QY 61 ggaatgctcaacaacggttactgttggaaacaacccgacagagtaacacccaaggaa 120
DB 61 GGATGCTCAACAACGTTACTGTGGAACAACCGACAGCATACCAAGAA 120
QY 121 accatcctcattcttcttctgttcgggaattggacaagaaacgttgatgcagcc 180
DB 121 ACCATCCTCATCTTCTTCTGTTCGGGAATGGACAAGAAACGTTGATGCAGCC 180
QY 181 aaattgtgagcggtgcagaaatgttcttaaacagaaactcagcaacattcgtaaat 240
DB 181 AAATTTGTGGCGGTGCAGAAATGTGTAAAAACAGAACTCAGCAAACTTCGTAAT 240
QY 241 ggaatgctcggtttatcacttcttgatcactatcccgctggaagccgggtatattgc 300
DB 241 GGATGCTCGGTTTATCATCTTTGCGATCTATCTCGCTGGAAGCCGGGTATATTGC 300
QY 301 tcacaatag 309
DB 301 TCACAATAG 309

RESULT 3

US-09-023-221A-21
Sequence 21, Application US/09023221A
Patent No. 6087128

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-21

Query Match 100.0%; Score 309; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 5,8e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgagagataataagatgaaataatgtttttctgcgcgtctggaagatcattataca 60
DB 34 ATGCAGGTAATAAGATGAAAAAATGTTATTTCTGCCGCTCGCAATGCTTATTACA 93

QY 61 ggaatgctcaacaacgcttactgtttggaacaacacgacagcagtaacccaagaagaa 120
DB 94 GGATGTCCTCAACAAAGCTTACTGTTGGAACAAACCGACAGCAATACCAACAAAGAA 153
QY 121 accatacctcaatcattcttcgttcggttggaatggacaagaagaactgttgaagcc 180
DB 154 ACCATACATCATATTCTTCTGTTGCGGAATGGACAAAGAAACTGTTGATGCAGCC 213
QY 181 aaatttggcgggtgcagaaatgttgaacaagaacacagcaaacatccgtaaat 240
DB 214 AAAATTGTCGCGTCGACAGAAATGTTTAAACAGAAACTCAGCAACATTCGTAAT 273
QY 241 ggaatcctcggttttactacttttgacatctatactccgttggaagccgggtatattgc 300
DB 274 GGATGTCGCTTTTATCACTTTTGGCATCTATACCTCGGTGGAAGCCGGGTATATTGC 333
QY 301 tcacaatag 309
DB 334 TCACAAATAG 342

RESULT 4

US-09-282-352A-21

Sequence 21, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

APPLICANT: ROBINSON, MICHAEL

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,352A

FILING DATE: 31-MAR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/023,221

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,0001010102

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 378 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-282-352A-21

Query Match 100.0%; Score 309; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 5.8e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atcagagataataagatgaagaaatgttattcttcgacgctctggcaatgctattaca 60
DB 1 atcagagataataagatgaagaaatgttattcttcgacgctctggcaatgctattaca 60

DB 34 ATCCAGATATAATAGTAAAAAATGTTATTTCTGCGCCTCTGCAATGCTTATTACA 93
QY 61 ggaatgctcaacaacgcttactgtttggaacaacacgacagcagtaacccaagaagaa 120
DB 94 GGATGTCCTCAACAAAGCTTACTGTTGGAACAAACCGACAGCAATACCAACAAAGAA 153
QY 121 accatacctcaatcattcttcgttcggttggaatggacaagaagaactgttgaagcc 180
DB 154 ACCATACATCATATTCTTCTGTTGCGGAATGGACAAAGAAACTGTTGATGCAGCC 213
QY 181 aaatttggcgggtgcagaaatgttgaacaagaacacagcaaacatccgtaaat 240
DB 214 AAAATTGTCGCGTCGACAGAAATGTTTAAACAGAAACTCAGCAACATTCGTAAT 273
QY 241 ggaatcctcggttttactacttttgacatctatactccgttggaagccgggtatattgc 300
DB 274 GGATGTCGCTTTTATCACTTTTGGCATCTATACCTCGGTGGAAGCCGGGTATATTGC 333
QY 301 tcacaatag 309
DB 334 TCACAAATAG 342

RESULT 5

US-09-023-221A-1

Sequence 1, Application US/09023221A
Patent No. 6087128

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,221A

FILING DATE: 12-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,0001010101

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 760 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-023-221A-1

Query Match 100.0%; Score 309; DB 3; Length 760;
Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atcagagataataagatgaagaaatgttattcttcgacgctctggcaatgctattaca 60
DB 292 ATCGAGATATAATAGTAAAAAATGTTATTTCTGCGCCTCTGCAATGCTTATTACA 351

QY 61 ggaatgctcaacaaagcttactgttggaacaaacagacagcaagtaacacaaagaa 120
|||||
DB 352 GGATGCTCTCAACAAAGTTACTGTGGAAACAAACGACAGATACACCAAGAA 411
QY 121 accatcaatcatcttctcgttcggaattgacaagaagaactgttgatgcagcc 180
|||||
DB 412 ACCATCATCATCTTCTCTTCGTTCCGGAAATTGGACAGAGAAACTGTGATGCAGCC 471
QY 181 aaatttgccggtgcagaaatgtgttaaaacagaactcagcaacattcgttaat 240
|||||
DB 472 AAAATTGTGGCGGTGACAGAAATGTGTAAACAGAACTCAGCAAACTTCGTAAT 531
QY 241 ggaatgctcggtttatcaacttttgcatctatactcgcgtggaagccggtatattgc 300
|||||
DB 532 GGATGCTCGGTTTATACACTTTTGCACTATACCTCCGCGAAGCCCGGGTATATTGC 591
QY 301 tcacaatag 309
|||||
DB 592 TCACAATAG 600

RESULT 6
US-09-282-352A-1
Sequence 1, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MOETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-282-352A-1

Query Match 100.0%; Score 309; DB 4; Length 760;
Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atcagagataaagaagaaataatgtttctcgcgctcgtggaatgctattaca 60
|||||

DB 292 ATGAGATATATAGATGAAAAATGTTATTTCTGCGCTCTGCAATGCTTATTACA 351
QY 61 ggaatgctcaacaaagcttactgttggaacaaacagacagcaagtaacacaaagaa 120
|||||
DB 352 GGATGCTCTCAACAAAGTTACTGTGGAAACAAACGACAGATACACCAAGAA 411
QY 121 accatcaatcatcttctcgttcggaattgacaagaagaactgttgatgcagcc 180
|||||
DB 412 ACCATCATCATCTTCTCTTCGTTCCGGAAATTGGACAGAGAAACTGTGATGCAGCC 471
QY 181 aaatttgccggtgcagaaatgtgttaaaacagaactcagcaacattcgttaat 240
|||||
DB 472 AAAATTGTGGCGGTGACAGAAATGTGTAAACAGAACTCAGCAAACTTCGTAAT 531
QY 241 ggaatgctcggtttatcaacttttgcatctatactcgcgtggaagccggtatattgc 300
|||||
DB 532 GGATGCTCGGTTTATACACTTTTGCACTATACCTCCGCGAAGCCCGGGTATATTGC 591
QY 301 tcacaatag 309
|||||
DB 592 TCACAATAG 600

RESULT 7
US-09-023-221A-5
Sequence 5, Application US/09023221A
Patent No. 6087128

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MOETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-023-221A-5

Query Match 88.4%; Score 273.2; DB 3; Length 309;
Best Local Similarity 96.8%; Pred. No. 3.2e-75;
Matches 309; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
QY 1 atcagagataaagaagaaataatgtttctcgcgctcgtggaatgctattaca 60
DB 1 atcagagataaagaagaaataatgtttctcgcgctcgtggaatgctattaca 60
|||||

QY 61 ggaatgctcaacaacgcttactgttggaaacaacagcagcaagtaacacccaagaa 120
DB 61 GGATGTCCTCAACAAGCTTACTGTGGAAACAACCGACAGAGTAACACCAAGGAA 120
QY 121 accatcaactcaatcttcttcggttcggaattggacaagaagaactgttgatgcagcc 180
DB 121 ACCATCACTCATATCTTCTTCTGTTCCCAATTGGAC-AGAGAAACTGTGTATGCAGCC 179
QY 181 aaatttg-tggcggtgcagaaatgtgttaaacagaactcagcaacttcgtaaa 239
DB 180 AAAATTGTGGCGGTGCAGAAAATGTGTAAACAGAACTCAGCAAACTTCGTAAA 239
QY 240 tggattgcggttttatactacttctgcatctactcgcgtggaagccgggtatattg 299
DB 240 TGCATTGCCGGGTTTATCTTGTGCACTATCTACTCCGGGAAACCCGTGTATATTG 299
QY 300 ctcaacatag 309
DB 300 CTCACAATAG 309

RESULT 8

US-09-282-352A-5

Sequence 5, Application US/09282352A

Patent No. 6187321

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

APPLICANT: ROBINSON, MICHAEL

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GEBHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,352A

FILING DATE: 31-MAR-1999

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 09/023,221

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,00010102

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-282-352A-5

DB 1 ATCAGAGTATATAGATGAAAAAATGTATTTTCGCCCTCTGCGCATGCTTATTACA 60
QY 61 ggaatgctcaacaacgcttactgttggaaacaacagcagcaagtaacacccaagaa 120
DB 61 GGATGTCCTCAACAAGCTTACTGTGGAAACAACCGACAGAGTAACACCAAGGAA 120
QY 121 accatcaactcaatcttcttcggttcggaattggacaagaagaactgttgatgcagcc 180
DB 121 ACCATCACTCATATCTTCTTCTGTTCCCAATTGGAC-AGAGAAACTGTGTATGCAGCC 179
QY 181 aaatttg-tggcggtgcagaaatgtgttaaacagaactcagcaacttcgtaaa 239
DB 180 AAAATTGTGGCGGTGCAGAAAATGTGTAAACAGAACTCAGCAAACTTCGTAAA 239
QY 240 tggattgcggttttatactacttctgcatctactcgcgtggaagccgggtatattg 299
DB 240 TGCATTGCCGGGTTTATCTTGTGCACTATCTACTCCGGGAAACCCGTGTATATTG 299
QY 300 ctcaacatag 309
DB 300 CTCACAATAG 309

RESULT 9

US-09-023-221A-6

Sequence 6, Application US/09023221A

Patent No. 6087128

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GEBHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,221A

FILING DATE: 12-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,00010101

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-023-221A-6

Query Match 88.4%; Score 273.2; DB 4; Length 309;
Best Local Similarity 96.8%; Pred. No. 5.2e-75;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
QY 1 atcagagatataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60
DB 1 atcagagatataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60

Query Match 81.6%; Score 252; DB 3; Length 309;
Best Local Similarity 88.6%; Pred. No. 1.7e-68;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 atcagagatataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60
DB 1 atcagagatataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60

Db 9535 ggaatgtctcggttttaattacttaggcattatattccgcgtgtaattgc 9590
|||||
QY 301 tcacaata 308
|||||
Db 9595 tcacaata 9602

```

RESULT 12
US-09-364-862-13
Sequence 13, Application US/09364862
Patent No. 6221349
GENERAL INFORMATION:
APPLICANT: Couto, Linda B.
APPLICANT: Colosl, Peter C.
TITLE OF INVENTION: ADEMO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
FILE REFERENCE: AVIGEN-03743
CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/1125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 11933
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-364-862-13

```

Query Match	81.6%	Score 252	DB 4	Length 11933
Best Local Similarity	86.6%	Pred. No. 6.6e-68		
Matches 273	Conservative	0	Mismatches 35	Indels 0
			Gaps	0
Qy	1 atgcagagataaagaagatgaaanaaatgttatcttcctgcgcgctctgccaatgtctattaca	60		
Db	9295 atcgggaataaacacatgnaaaaaaattgtcaccctgcactgcgtgcgtgcctgtctattaca	9354		
Qy	61 ggaatgtgtccaacaaacggttactcgttctgnaaacaaacgcagcagtaaacccaagaagaa	120		
Db	9355 ggaatgtgtccaacagacggttactcgttctcaaaaacaaacgcagcagtaaacccaagaagaa	9414		
Qy	121 acccaccatccatcatcttcttcgttcgcggaattgtgacaaagaanaaacttgaatgaagcc	180		
Db	9415 acccaccacccacatcttcttcgttcttcggaattgtgacaaagaanaaacttgcgatgaagcc	9474		
-Qy	181 aaaatcttgtcgcgctgacagaanaatctgtttaaacagaaacccagcaaaacatctgnaaat	240		
Db	9475 aaaatcttgtcgcgctgacagaanaatctgtttaaacagaaacccagcaaaacatctgnaaat	9534		
Qy	241 ggaatgtgtgcgttattacacacttgcgcacatactacactgcgcgtggaagcccggtatattgc	300		
Db	9535 ggaatgtgtgcgttattattacttactagcatcttatactactcgcgtggaagcgcgtgtattatgc	9594		
Qy	301 tccacaata 308			
Db	9595 tccacaata 9602			

```

RESULT 13
US-09-002-361-4
; Sequence 4, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Black
; TITLE OF INVENTION: Lepidopteran GABA-gated Chloride
; TITLE OF INVENTION: Channels

```

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002.361
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1443
OTHER INFORMATION:
US-09-002-361-4

	Query Match	Similarity	11.1%	Score 34.2;	DB 4;	Length 1519;	
	Best Local	Similarity	67.6%	Pred. No. 0.21;	23;	Indels	0;
Oy	Matches	48;	Conservative	0;	Mismatches		
Oy	153	tggacagagaanaactgtttgatgcagccaaattcttgcgctgacgaanaatgtyttaa	212				
Dd	992	TGGCAAAAGATTAAGATGACAAAAACAAGAATTGTGGCCATACAGAAAATAGCTTCTG	1051				
Oy	213	aacagaactc	223				
Dd	1052	AAAAGAAATC	1062				

RESULT 14
 US-08-743-637B-1
 : Sequence 1, Application US/08743637B
 : Patent No. 5994066
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: BERGERON, Michel G.
 : APPLICANT: PICARD, Francois J.
 : APPLICANT: OUELLETTE, Marc
 : APPLICANT: ROY, Paul H.
 :
 : TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
 : TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
 : TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
 : TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ..
 :
 : NUMBER OF SEQUENCES: 273
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CHARLES & BRADY
 : STREET: 411 EAST WISCONSIN AVENUE
 : CITY: MILWAUKEE
 : STATE: WISCONSIN

COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
US-08-743-637B-1

Query Match 10.9%; Score 33.6; DB 2; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.34; Mismatches 74; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy 127 acatcatcttccttcggttcggaattgacaagaagaactgtgtatgcagccaatt 186
Db 1211 ACATATCTCTCCTTTAGATGTAGTGTGCATGAATGACACATGCTGTGACGGAACAT 1270
Qy 187 tctggcgggtgcagaagaattgtttaaaacagaaactcagcaaacattcgttaattgattg 246
Db 1271 ACTGCCGCTTAGAATATTAGACAAATCAGATGCTTGAATGAATCTTATTCTGATTGG 1330
Y 247 ctgggtttatcaactttggcatctatcc 278
Db 1331 ATGGGTATTATTATTGGGTCATCTAATCC 1362

RESULT 15
US-08-526-840B-1
Sequence 1, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
US-08-526-840B-1

Query Match 10.9%; Score 33.6; DB 3; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.34; Mismatches 74; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy 127 acatcatcttccttcggttcggaattgacaagaagaactgtgtatgcagccaatt 186
Db 1211 ACATATCTCTCCTTTAGATGTAGTGTGCATGAATGACACATGCTGTGACGGAACAT 1270
Qy 187 tctggcgggtgcagaagaattgtttaaaacagaaactcagcaaacattcgttaattgattg 246
Db 1271 ACTGCCGCTTAGAATATTAGACAAATCAGATGCTTGAATGAATCTTATTCTGATTGG 1330
Qy 247 ctgggtttatcaactttggcatctatcc 278
Db 1331 ATGGGTATTATTATTGGGTCATCTAATCC 1362

Search completed: July 23, 2002, 13:45:10
Job time: 5111 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:51:26 ; Search time 365.82 Seconds

(Without alignments)
1450.239 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309
Sequence: 1 atgcagcataataagatgaa.....gggtatatgtctcacaatg 309

Indexing table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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23: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	309	100.0	309	AAA73698	Avian Escherichia
2	309	100.0	309	AAFS8100	Avian E coli Isola
3	309	100.0	378	AAA73697	E.coli ISS gene in
4	309	100.0	309	AAFS8800	Avian E coli Isola
5	309	100.0	760	AAA73681	Avian Escherichia
6	309	100.0	760	AAFS8784	Avian E coli Isola
7	273.2	88.4	309	AAA73684	Iss cDNA from a se
8	273.2	88.4	309	AAFS8787	Human E coli Isola
9	252	81.6	309	AAA73685	Lambda Bor gene.

10	252	81.6	309	AAFS8788	Phage lambda bor g
11	252	81.6	11933	AAFD0121	Recombinant adeno
12	252	81.6	11933	AAFD0612	Human factor VIII
13	141.6	45.8	180	ABAB8818	Escherichia coli p
14	36.2	11.7	1685	AAAS9393	DNA encoding novel
15	36.2	11.7	1685	AAAS9393	Candida albicans p
16	36.2	11.7	1685	AAAS9393	Streptococcus pyog
17	35.2	11.4	4951	AAAI3198	Enterococcus faec
18	34.2	11.1	1519	AAI64373	GABA-gated chlorid
19	34.2	11.1	1519	AAI64373	E. faecalis detect
20	33.6	10.9	1817	ABAT8345	Enterococcus faeca
21	33.6	10.9	1817	ABAT8345	Drosophila melanog
22	33.6	10.9	1817	ABAT8345	Nucleic acid seque
23	33.6	10.7	1263	AAAC3008	Arabidopsis thalia
24	33.6	10.7	1263	AAAC3008	Arabidopsis thalia
25	32.8	10.6	4380	AAAN91839	Pasteurella multoc
26	32.8	10.6	4380	AAAN91839	Pasteurella multoc
27	32.8	10.6	6272	AAAV74451	Staphylococcus aur
28	32.6	10.6	1727	AAAX20147	Enterococcus faeca
29	32.6	10.6	1839	AAAX20146	Enterococcus faeca
30	32.6	10.6	7657	AAAI2970	Enterococcus faeca
31	32.4	10.5	1924	AAQ80002	ADP-glucose-pyroph
32	32.4	10.5	106416	ABLI8718	Drosophila melanog
33	32.2	10.4	408	AAZ80085	Human colon cancer
34	32.2	10.4	1690	AAQ92524	Nicotiana glauca
35	32.2	10.4	2364	AAAF7837	Glycerol dehydrata
36	32.2	10.4	4963	AAAF7841	Fragment of Clostr
37	32	10.4	344	AAAC21119	Human secreted pro
38	32	10.4	73334	ABLI4125	S. epidermidis ope
39	31.8	10.3	1470	AAH53837	S. epidermidis ope
40	31.8	10.3	1470	AAH53837	S. epidermidis ope
41	31.8	10.3	2754	AAK00552	Human immune/haema
42	31.8	10.3	3233	AAH54222	S. epidermidis gen
43	31.8	10.3	3249	AAH54258	S. epidermidis gen
44	31.8	10.3	3511	AAH54566	S. epidermidis gen
45	31.8	10.3	6034	ABLI2986	Drosophila melanog

ALIGNMENTS

RESULT 1	AAA73698	standard; DNA; 309 BP.
ID	AAA73698	
XX	AAA73698	
AC	AAA73698	
XX	07-DEC-2000	(first entry)
DT	07-DEC-2000	
XX	Avian Escherichia coli	ISS cDNA.
DE	Avian Escherichia coli	ISS cDNA.
XX	Iss: avian; Outer membrane protein; OMP; vaccine; antibacterial;	
KW	avian colibacillosis; septicemic; psex-CP-3; ss.	
XX	Escherichia coli.	
OS	Escherichia coli.	
XX	Key	Location/Qualifiers
FF	CDS	1..309
FT	CD	/tag- a
FT	CD	/product= Iss
XX	US6087128-A.	
PN	US6087128-A.	
XX	11-JUL-2000.	
PD	11-JUL-2000.	
XX	12-FEB-1998;	98US-0023221.
PF	12-FEB-1998;	98US-0023221.
XX	12-FEB-1998;	98US-0023221.
PR	12-FEB-1998;	98US-0023221.
XX	(NDSU-) NDSU RES FOUND.	
PA	(NDSU-) NDSU RES FOUND.	
XX	Nolan LK, Horne SM;	
XX	Nolan LK, Horne SM;	
PI	Nolan LK, Horne SM;	
XX	Nolan LK, Horne SM;	

DR WPI: 2000-531343/48.
 DR P-PSDB: AAB14981.

XX Nucleic acid molecule encoding *iss* polypeptide isolated from avian
 PT *Escherichia coli*, used to prevent avian septicemic diseases and for
 PT diagnostic and control strategies for avian colibacillosis

XX Claim 17, Fig 3; 33pp; English.

XX The present invention relates to the avian *Escherichia coli iss* gene.
 CC *iss* encodes an outer membrane protein. This gene was obtained by PCR
 CC amplification of an *E. coli* isolate from chick serum. The present
 CC sequence is the *iss* cDNA as cloned in frame into the expression vector
 CC pGEX-6P-3. The *iss* gene is useful as a vaccine for treating and
 CC preventing avian septicemic diseases and functions as a marker for
 CC diseases causing avian *E. coli* infection. This forms the basis for
 CC improved diagnostic and control strategies for avian colibacillosis.

XX Sequence 309 BP; 101 A; 60 C; 64 G; 84 T; 0 other;

Query Match 100.0%; Score 309; DB 21; Length 309;
 Best Local Similarity 100.0%; Pred. No. 8.4e-80;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atcgagataataagatgataaaatgttatttctgcgcctctgcaatgctattaca 60
 Db 1 atcgagataataagatgataaaatgttatttctgcgcctctgcaatgctattaca 60
 QY 61 ggaatgctcaaaaacggttactgttggaaacacccgacagcaagtaacacaaagaa 120
 Db 61 ggaatgctcaaaaacggttactgttggaaacacccgacagcaagtaacacaaagaa 120
 QY 121 accatcaatcatcattctcttcggttcggaattggacaagaagaactgttgatgacgc 180
 Db 121 accatcaatcatcattctcttcggttcggaattggacaagaagaactgttgatgacgc 180
 QY 181 aaattctggcggtgcagaaaatgtgttaaaacagaaactcagcaaacattcgttaaat 240
 Db 181 aaattctggcggtgcagaaaatgtgttaaaacagaaactcagcaaacattcgttaaat 240
 QY 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 Db 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 QY 301 tcacaataag 309
 Db 301 tcacaataag 309

RESULT 2

AA58100
 ID AAF58100 standard; DNA; 309 BP.

XX AAF58100;

XX 04-MAY-2001 (first entry)

DE Avian *E. coli* isolate *iss* gene clone SEQ ID NO: 22.

XX Avian *E. coli* infection; respiratory tract lesion; septicemia;

XX colibacillosis; ds.

XX *Escherichia coli*.

XX US6187321-B1.

XX 13-FEB-2001.

XX 31-MAR-1999; 99US-0282352.

XX 12-FEB-1998; 98US-0023221.

PA (UYND-) UNIV NORTH DAKOTA STATE.

XX Nolan LK, Horne SM, Robinson M;

XX WPI: 2001-190978/19.

DR Novel isolated and purified avian *Escherichia coli iss* polypeptide

XX useful for treating *Escherichia coli* infection selected from

XX colibacillosis, coliformuloma, peritonitis, salpingitis, synovitis,

XX omphalitis

XX Example 2; Column 47-48; 35pp; English.

XX The present invention provides the protein and coding sequences of the

XX *Escherichia coli iss* protein. This can be used in the diagnosis and

XX treatment of, and vaccines against, *E. coli* infection in domestic birds,

XX where the bacterium causes septicemia, respiratory tract lesions and

XX colibacillosis.

SQ Sequence 309 BP; 101 A; 60 C; 64 G; 84 T; 0 other;

Query Match 100.0%; Score 309; DB 22; Length 309;
 Best Local Similarity 100.0%; Pred. No. 8.4e-80;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atcgagataataagatgataaaatgttatttctgcgcctctgcaatgctattaca 60
 Db 1 atcgagataataagatgataaaatgttatttctgcgcctctgcaatgctattaca 60
 QY 61 ggaatgctcaaaaacggttactgttggaaacacccgacagcaagtaacacaaagaa 120
 Db 61 ggaatgctcaaaaacggttactgttggaaacacccgacagcaagtaacacaaagaa 120
 QY 121 accatcaatcatcattctcttcggttcggaattggacaagaagaactgttgatgacgc 180
 Db 121 accatcaatcatcattctcttcggttcggaattggacaagaagaactgttgatgacgc 180
 QY 181 aaattctggcggtgcagaaaatgtgttaaaacagaaactcagcaaacattcgttaaat 240
 Db 181 aaattctggcggtgcagaaaatgtgttaaaacagaaactcagcaaacattcgttaaat 240
 QY 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 Db 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 QY 301 tcacaataag 309
 Db 301 tcacaataag 309

RESULT 3

AA73697
 ID AAA73697 standard; DNA; 378 BP.

XX AAA73697;

XX 07-DEC-2000 (first entry)

DE *E. coli iss* gene in expression vector pGEX-6P-3.

XX *iss*; avian; outer membrane protein; OMP; vaccine; antibacterial;

XX avian colibacillosis; septicemic; pGEX-6P-3; ss.

XX *Escherichia coli*.

XX Key Location/Qualifiers

XX CDS 34..342

XX FT /*tag= a

XX FT /product= iss

XX US6087128-A.

PD		11-JUL-2000.
XX		
PP	12-FEB-1998;	98US-0023221.
XX		
PR	12-FEB-1998;	98US-0023221.
XX		
PA	(NDSU-) NDSU RES FOUND.	
XX		
PJ	Nolan LK, Horne SM,	
XX		
DR	WPI: 2000-531343/48.	
DR	P-PsDE; AAB1984.	
XX		
PT	Nucleic acid molecule encoding Iss polypeptide isolated from avian Escherichia coli, used to prevent avian septicemic diseases and for diagnostic and control strategies for avian colibacillosis - -	
PS	Disclosure; Fig 3; 33pp; English.	
CC	The present invention relates to the avian Escherichia coli iss gene iss encodes an outer membrane protein. This gene was obtained by PCR amplification of an E.coli isolate from chick serum. The present sequence is the iss gene cloned in frame into the expression vector pcgX-GP-3. The iss gene is useful as a vaccine for treating and preventing avian septicemic diseases and functions as a marker for diseases causing avian E. coli infection. This forms the basis for improved diagnostic and control strategies for avian colibacillosis. -	
XX		
SQ	Sequence 378 BP; 112 A; 80 C; 84 G; 102 T; 0 other;	

Query Match	100.0%	Score 309	DB 21	length 378
Best Local Similarity	100.0%	Pred. NO	8.9e-80	
Matches 309	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	atgcaaggtaataagaatgaaaaaaaatcttatcttcgcgcctcggaatgctattaca	60
QY	34	atgcaggataataagaatgaaaaaaaatgtattcttcgcgcctcggaatgctattaca <td>93</td>	93
DB			
QY	61	ggatgtgtctcaacaaacggttactcgtttggaaaacaacccgacagcagtaatacaccaaaagaa <td>120</td>	120
DB	94	ggatgtgtctcaacaaacggttactcgtttggaaaacaacccgacagcagtaatacaccaaaagaa <td>153</td>	153
QY	121	accatcactcatcatcttccttcggttcggaaatgagacaagaagaaactgtgtatgcagcc <td>180</td>	180
DB	154	accatcactcatcatcttccttcggttcggaaatgagacaagaagaaactgtgtatgcagcc <td>213</td>	213
QY	181	aaaatttgtgcggttcgcagaaaatggttgttaaaaacaaactcagcaaacatctcgttaaat <td>240</td>	240
DB	214	aaaatttgtgcggttcgcagaaaatggttgttaaaaacaaactcagcaaacatctcgttaaat <td>273</td>	273
QY	241	ggattgcgcggttttatacaactttgtgcatactatccgcgttcggaagccgggtatattgc <td>300</td>	300
DB	274	ggattgcgcggttttatacaactttgtgcatactatccgcgttcggaagccgggtatattgc <td>333</td>	333
QY	301	tcacaaatg 309	
DB	334	tcacaaatg 342	

```

RESULT      4
AAF58800
ID   AAF58800 standard; DNA; 378 BP.

```

AC AAF58800

DT 04-MAY-2001 (first entry)

DE Avian E coli isolate protease cleavage site DNA SEQ ID NO: 21.

KW Avian E coli infection; respiratory tract lesion; septicaemia;

XX

OS Escherichia coli.
XX
XX US6187321-B1.
PN
XX 13-FEB-2001.
PD
XX 31-MAR-1999; 99US-0282352.
PF
XX 12-FEB-1998; 98US-0023221.
PR
XX (UYND-) UNIV NORTH DAKOTA STATE.
PA
XX Nolan LK, Horne SM, Robinson M;
PI
XX WPI: 2001-190978/19.
DR P-PSDB: AAB69397.
PT
XX Novel isolated and purified avian Escherichia coli iss polypeptide
PT useful for treating Escherichia coli infection selected from
PT colibacillosis, collagenoma, peritonitis, salpingitis, synovitis,
PT omphalitis
PS
XX Example 2: Column 47-48; 35pp; English.

The present invention provides the protein and coding sequences of the
CC Escherichia coli iss protein. This can be used in the diagnosis and
CC treatment of, and vaccines against, E. coli infection in domestic birds
CC where the bacterium causes septicaemia, respiratory tract lesions and
CC colibacillosis.
XX

Sequence 378 BP; 112 A; 80 C; 84 G; 102 T; 0 other;

50 Sequence 378 BP; 112 A; 80 C; 84 G; 102 T; 0 other;

	Query Match	100.0%	Score 309:	DB 22:	Length 378:	
	Best Local Similarity	100.0%:	Pred. NO.	8.9e-80:		
	Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0:	
QY	1 atgcgagataatgaatgaaaaaaattgtattttcttcgccgcctcgtcgcaatgtattaca	60				
Db	34 atgcggagataaaaagtgaaaaaaatgtattttcttcgccgcctcgtcgcaatgtattaca	93				
QY	61 ggaatgtctcaacaaacgttctactcttgcgaaacaaaccgcagccagtaaacacaaaggaa	120				
Db	94 ggaatgtctcaacaaacgcttactcttgcgaaacaaaccgcagccagtaaacacaaaggaa	153				
QY	121 accacactcatcattttcttcgttcggagaatttgacagaagaaaacctgttatcgagcc	180				
Db	154 accacactcatcattttcttcgttcggagaatttgacagaagaaaacctgtgtatcgagcc	213				
QY	181 aaaatttgtgcggtgcagaaaatgttctttaaacagaagaaccgcagaacattcgttaat	240				
Db	214 aaaatttgtgcggtgcagaaaatgttctttaaacagaagaaccgcagaacattcgttaat	273				
QY	241 ggatgtcgtcggtttatcaactttcggcatctatactcgcgtcgyaaGCCGGTatatc	300				
Db	274 ggatgtcgtcggtttatcaacttttgcatactatactcgcgtcgyaaGCCGGTatatc	333				
QY	301 tccacatag 309					
Db	334 tccacatag 342					

```

RESULT      5
AAA73681
ID   AAA73681 standard; DNA; 760 BP.

```

AC AAA73681

DT 07-DEC-2000 (first entry)

DE Avian Escherichia coli 1ss gene.

KW Ibs; avian; outer membrane protein; OMP; vaccine; antibacterial;

XX	avian colibacillosis; septicemic; ds.
XX	
OS	Escherichia coli.
XX	
XX	Key
XX	Location/Qualifiers
FT	292..600
FT	/*tag= a
FT	/product= "iss"
XX	
XX	US6087128-A.
XX	
PD	11-JUL-2000.
XX	
XX	12-FEB-1998; 98US-0023221.
XX	
PR	12-FEB-1998; 98US-0023221.
XX	
XX	(NDSU-) NDSU RES FOUND.
XX	
XX	Nolan LK, Horne SM;
XX	
XX	WPI: 2000-531343/48.
DR	
DR	P-PSDB; AAB14981.
XX	
XX	Nucleic acid molecule encoding iss polypeptide isolated from avian
PT	Escherichia coli, used to prevent avian septicemic diseases and for
PT	diagnostic and control strategies for avian colibacillosis
XX	
PS	Claim 2, Column 35-38; 33pp; English.
XX	
CC	The present sequence is the avian Escherichia coli iss gene. iss
CC	encodes an outer membrane protein. This gene was obtained by PCR
CC	amplification of an E.coli isolate from chick serum. The primers used
CC	are shown in AAA73682 and AAA73683. The iss gene is useful as a vaccine
CC	for treating and preventing avian septicemic diseases and functions
CC	as a marker for diseases causing avian B. coli infection. This forms
CC	the basis for improved diagnostic and control strategies for avian
CC	colibacillosis.
XX	
XX	Sequence 760 BP; 216 A; 159 C; 160 G; 225 T; 0 other;

Query Match	Similarity	100.0%	Score 309:	DB 21:	Length 760:
Best Local	Similarity	100.0%	Pred. NO. 1.1e-75:		
Matches 309:	Conservative	0:	Mismatches	0:	Indels
					Gaps
					0:
1	atcgaggaataaagatgtaaaaaaatgtattttcttctgcgcctctgccaatgtattaca	60			
292	atgcggagtaataagatgtaaaaaaatgtattttcttctgcgcctctgccaatgtattaca	351			
QY	61 ggaatgctcaacaacgctttactctgttggaaaacaacgcagcaagtaaccacaaggaa	.120			
Db	352 ggaatgctcaacaacgctttactctgttggaaaacaacgcagcaagtaaccacaaggaa	411			
QY	121 accatcactcatcattctcttccttcgggaattggacaagagaanaactgttatgcagcc	180			
Db	412 accatcactcatcattctcttccttcgggaattggacaagagaanaactgttatgcagcc	471			
QY	181 aaattctgtgcggtgcagaaaaatgttgttaaaacagaaactcagcaaacattcgttaat	240			
Db	472 aaattctgtgcggtgcagaaaaatgttgttaaaacagaaactcagcaaacattcgttaat	531			
QY	241 ggattgcgcggtttatataactttggcatcttaactccgctggaagcccggtatatctgc	300			
Db	532 ggattgcgcggtttatataactttggcatcttaactccgctggaagcccggtatatctgc	591			
QY	301 tcacacatag 309				
Db	592 tcacacatag 600				

XX	AAE58784 standard; DNA; 760 BP.
XX	AAE58784;
XX	
XX	04-MAY-2001 (first entry)
XX	
XX	Avian E coli isolate 1as gene SEQ ID NO: 1.
XX	
XX	Avian E coli infection; respiratory tract lesion; septicaemia;
XX	colibacillosis; ds.
XX	
XX	Escherichia coli.
XX	
XX	US6187321-B1.
XX	
XX	13-FEB-2001.
XX	
XX	31-MAR-1999; 99US-0282352.
XX	
XX	12-FEB-1998; 98US-0023221.
XX	
XX	(UYND-) UNIV NORTH DAKOTA STATE.
XX	
XX	
XX	Noian LK, Horne SM, Robinson M;
XX	
XX	WPI: 2001-190978/19.
XX	
XX	P-PSDB; AAB69394.
XX	
XX	Novel isolated and purified avian Escherichia coli 1as polypeptide
XX	useful for treating Escherichia coli infection selected from
XX	colibacillosis, coligranuloma, peritonitis, salpingitis, synovitis,
XX	omphalitis
XX	
XX	Example 1; Column 37-38; 35pp; English.
XX	
XX	The present invention provides the protein and coding sequences of the
XX	Escherichia coli 1as protein. This can be used in the diagnosis and
XX	treatment of, and vaccines against, E. coli infection in domestic birds,
XX	where the bacterium causes septicaemia, respiratory tract lesions and
XX	colibacillosis.
XX	
XX	Sequence 760 BP; 216 A; 159 C; 160 G; 225 T; 0 other;

	Query Match	100.0%	Score 309	DB 22	Length 760
	Best Local Similarity	100.0%	Pred. NO. 1.1e-79		
	Matches 309	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 atcgagataataagatgataaaaaaagtattattttctgcgcgcctgycgaatgtattaca	60			
Db	292 atcgagataataagatgataaaaaaagtattattttctgcgcgcctgycgaatgtattaca	351			
QY	61 ggaatgctcaacaacgcttacctgttggaaacaacacgacagcgtaacaccaaagaa	120			
Db	352 ggaatgctcaacaacgcttacctgttggaaacaacacgacagcgtaacaccaaagaa	411			
QY	121 accactactatcatcttcttcgttcgggaatgtgaaacagagaanaaaactgtatcagac	180			
Db	412 accactactatcatcttcttcgttcgggaatgtgaaacagagaanaaaactgtatcagac	471			
QY	181 aaattctgacggtgcagaaatgtctttaaacaagaaacccagacaaacattcgttaaat	240			
Db	472 aaattctgacggtgcagaaatgtctttaaacaagaaacccagacaaacattcgttaaat	531			
QY	241 ggaatgctcgatttaccactttggaactctatactcgcgtgaaagcccggtatattgc	300			
Db	532 ggaatgctcgatttaccactttggaactctatactcgcgtgaaagcccggtatattgc	591			
QY	301 tcacaaatg 309				
Db	592 tcacaaatg 600				

RESULT 7
 AAA73684 standard; cDNA; 309 BP.
 ID AAA73684
 AC AAA73684;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Iss cDNA from a septicemic human E.coli isolate.
 XX
 KM Iss; avian; outer membrane protein; OMP; vaccine; antibacterial;
 XX avian colibacillosis; septicemic; human; ss.
 XX
 OS Escherichia coli.
 XX
 Key Location/Qualifiers
 CDS 1..309
 /*tag- a
 /product- Iss
 US6087128-A.
 11-JUL-2000.
 12-FEB-1998; 98US-0023221.
 12-FEB-1998; 98US-0023221.
 (NDSU-) NDSU RES FOUND.
 Nolan LK, Horne SM;
 WPI: 2000-531343/48.
 P-PSDB: AAB14982.
 Nucleic acid molecule encoding Iss polypeptide isolated from avian Escherichia coli, used to prevent avian septicemic diseases and for diagnostic and control strategies for avian colibacillosis
 PS Disclosure; Fig 1; 33pp; English.
 XX
 CC The present invention relates to the avian Escherichia coli Iss gene.
 CC Iss encodes an outer membrane protein. This gene was obtained by PCR
 CC amplification of an E.coli isolate from chick serum. The present
 CC sequence is the Iss gene from a septicemic human E.coli isolate,
 CC which shows homology to the avian E. coli Iss gene. The Iss
 CC gene is useful as a vaccine for treating and preventing avian
 CC septicemic diseases and functions as a marker for diseases causing
 CC avian E. coli infection. This forms the basis for improved diagnostic
 CC and control strategies for avian colibacillosis.
 XX
 Sequence 309 BP; 101 A; 65 C; 59 G; 84 T; 0 other;
 Query Match 88.4%; Score 273.2; DB 21; Length 309;
 Best Local Similarity 96.8%; Pred. NO. 1.9e-69;
 Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
 OY 1 atgcagataataagatgaataaagtattttctgcgcgtctggaatgtatttata 60
 DB 1 atgcagataataagatgaataaagtattttctgcgcgtctggaatgtatttata 60
 OY 61 ggaatgtctcaacaacagttactctgttgaaacaacacgacgacgttaacacaaagaa 120
 DB 61 ggaatgtctcaacaacagttactctgttgaaacaacacgacgacgttaacacaaagaa 120
 OY 121 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 180
 DB 121 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 180
 OY 122 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 179
 DB 122 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 179
 OY 181 aaatttg-tggcgggtgcagaaagtgttttaaacagaagaactcgcaaacattgtataa 239
 DB 181 aaatttg-tggcgggtgcagaaagtgttttaaacagaagaactcgcaaacattgtataa 239
 DB 180 aaatttg-tggcgggtgcagaaagtgttttaaacagaagaactcgcaaacattgtataa 239

RESULT 8
 AAF58787 standard; DNA; 309 BP.
 ID AAF58787
 AC AAF58787;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Human E coli isolate Iss gene SEQ ID NO: 5.
 XX
 DE Human E coli isolate; respiratory tract lesion; septicemia;
 XX Avian E coli infection; respiratory tract lesion; septicemia;
 XX colibacillosis; ds.
 XX
 OS Escherichia coli.
 XX
 OS Escherichia coli.
 XX
 XX US6187321-B1.
 13-FEB-2001.
 31-MAR-1999; 99US-0282352.
 12-FEB-1998; 98US-0023221.
 (UYND-) UNIV NORTH DAKOTA STATE.
 Nolan LK, Horne SM, Robinson M;
 WPI: 2001-190978/19.
 Novel isolated and purified avian Escherichia coli Iss polypeptide
 PT useful for treating Escherichia coli infection selected from
 PT colibacillosis, coligranuloma, peritonitis, salpingitis, synovitis,
 PT omphalitis
 PS Example 1; Column 39-40; 35pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC Escherichia coli Iss protein. This can be used in the diagnosis and
 CC treatment of, and vaccines against, E. coli infection in domestic birds,
 CC where the bacterium causes septicemia, respiratory tract lesions and
 CC colibacillosis.
 CC
 XX
 Sequence 309 BP; 101 A; 65 C; 59 G; 84 T; 0 other;
 Query Match 88.4%; Score 273.2; DB 22; Length 309;
 Best Local Similarity 96.8%; Pred. NO. 1.9e-69;
 Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
 OY 1 atgcagataataagatgaataaagtattttctgcgcgtctggaatgtatttata 60
 DB 1 atgcagataataagatgaataaagtattttctgcgcgtctggaatgtatttata 60
 OY 61 ggaatgtctcaacaacagttactctgttgaaacaacacgacgacgttaacacaaagaa 120
 DB 61 ggaatgtctcaacaacagttactctgttgaaacaacacgacgacgttaacacaaagaa 120
 OY 121 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 180
 DB 121 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 180
 OY 122 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 179
 DB 122 accatcactcatcattctctcgttttcgggaattggacaagaagaaactgtgatgcagcc 179
 OY 181 aaatttg-tggcgggtgcagaaagtgttttaaacagaagaactcgcaaacattgtataa 239
 DB 181 aaatttg-tggcgggtgcagaaagtgttttaaacagaagaactcgcaaacattgtataa 239

```

Db 180 aaattgtgtggtgcagaaatgtgttaaaacagaaactcagcaaacattcgttaa 239
Qy 240 tgaattgtcgtgtttatcaactttgtgcatctatatactcgcgtggaagccggtatattg 299
Db 240 tgaattgtcgtgtttatcaactttgtgcatctatatactcgcgtggaagccggtatattg 299
Qy 300 ctcaacaatag 309
Db 300 ctcaacaatag 309

RESULT 9
AAA73685
ID AAA73685 standard; DNA; 309 BP.
AC AAA73685;
XX
XX 07-DEC-2000 (first entry)
XX
XX Lambda Bor gene.
XX
XX Iss; avian; outer membrane protein; OMP; vaccine; antibacterial;
XX avian colibacillosis; septicemic; lambda; bor; ds.
XX
XX Bacteriophage lambda.
XX
XX Key Location/Qualifiers
XX CDS 16..309
XX /*tag= a
XX /product= Bor
XX
XX US6087128-A.
XX
XX 11-JUL-2000.
XX
XX 12-FEB-1998; 98US-0023221.
XX
XX 12-FEB-1998; 98US-0023221.
XX
XX (NDSU-) NDSU RES FOUND.
XX
XX Nolan LK, Horne SM;
XX
XX WPI; 2000-531343/48.
XX
XX P-PSDB; AABI4983.
XX
XX Nucleic acid molecule encoding iss polypeptide isolated from avian
XX Escherichia coli, used to prevent avian septicemic diseases and for
XX diagnostic and control strategies for avian colibacillosis
XX
XX Disclosure; Fig 1; 33pp; English.
XX
XX The present invention relates to the avian Escherichia coli iss gene.
XX iss encodes an outer membrane protein. This gene was obtained by PCR
XX amplification of an E.coli isolate from chick serum. The present
XX sequence is the lambda bor gene, which shows homology to the avian
XX E. coli iss gene. The iss gene is useful as a vaccine for treating
XX CC and preventing avian septicemic diseases and functions as a marker
XX CC for diseases causing avian E. coli infection. This forms the basis
XX CC for improved diagnostic and control strategies for avian colibacillosis.
XX
XX Sequence 309 BP; 97 A; 69 C; 65 G; 78 T; 0 other;

Query Match 81.6%; Score 252; DB 21; Length 309;
Best Local Similarity 88.6%; Pred. No. 2.5e-63;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 atgcagataataagatgaanaaatgtattttctgcgcgtctggcaatgctattaca 60
Db 1 atgcagataataagatgaanaaatgtattttctgcgcgtctggcaatgctattaca 60
Qy 61 ggaatgtgtcgaacacatgataaaatgtctactcgtctactggtgcccgtattata 60

```

```

Db 61 ggaatgtgtcgaacacatgataaaatgtctactcgtctactggtgcccgtattata 60
Qy 121 accatcaatcaatctcttctgttcgggaattggacaagaanaactgttgaatgcagcc 180
Db 121 accatcaatcaatctcttctgttcgggaattggacaagaanaactgttgaatgcagcc 180
Qy 181 aaattgtgtcgtgtgcagaaatgtgttaaaacagaaactcagcaaacattcgttaat 240
Db 181 aaattgtgtcgtgtgcagaaatgtgttaaaacagaaactcagcaaacattcgttaat 240
Qy 241 ggaatgtcgtgtttatcaactttgtgcacatatactcgcgtggaagccggtatattgc 300
Db 241 ggaatgtcgtgtttatcaactttgtgcacatatactcgcgtggaagccggtatattgc 300
Qy 301 tcacaata 308
Db 301 tcacaata 308

RESULT 10
AAF58768
ID AAF58768 standard; DNA; 309 BP.
AC AAF58768;
XX
XX 04-MAY-2001 (first entry)
XX
XX Phage lambda bor gene SEQ ID NO: 6.
XX
XX Avian E coli infection; respiratory tract lesion; septicaemia;
XX colibacillosis; ds.
XX
XX Bacteriophage lambda.
XX
XX US6187321-B1.
XX
XX 13-FEB-2001.
XX
XX 31-MAR-1999; 99US-0282352.
XX
XX 12-FEB-1998; 98US-0023221.
XX
XX (UNIV-) UNIV NORTH DAKOTA STATE.
XX
XX Nolan LK, Horne SM, Robinson M;
XX
XX WPI; 2001-190978/19.
XX
XX Novel isolated and purified avian Escherichia coli iss polypeptide
XX useful for treating Escherichia coli infection selected from
XX colibacillosis, coligranuloma, peritonitis, salpingitis, synovitis,
XX omphalitis
XX
XX Example 1; Column 39-40; 35pp; English.
XX
XX The present invention provides the protein and coding sequences of the
XX Escherichia coli iss protein. This can be used in the diagnosis and
XX treatment of, and vaccines against, E. coli infection in domestic birds,
XX where the bacterium causes septicaemia, respiratory tract lesions and
XX colibacillosis.
XX
XX Sequence 309 BP; 97 A; 69 C; 65 G; 78 T; 0 other;

Query Match 81.6%; Score 252; DB 22; Length 309;
Best Local Similarity 88.6%; Pred. No. 2.5e-63;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 atgcagataataagatgaanaaatgtattttctgcgcgtctggcaatgctattaca 60
Db 1 atgcagataataagatgaanaaatgtattttctgcgcgtctggcaatgctattaca 60

```


QY 61 ggaatgctcaacaaacgttactgttggaaacacacgacgagtaaccacaaagaa 120
 Db 61 ggaatgctcaacaaacgttactgttggaaacacacgacgagtaaccacaaagaa 120
 QY 121 accatcaccatcattcttcgttccggaattgacagaagaacctgtgatgagcc 180
 Db 121 accatcaccatcattcttcgttccggaattgacagaagaacctgtgatgagcc 180
 QY 181 aaatttggcgcgtgcagaaaatgtgttaaacagaaacacacacacatcgtaaat 240
 Db 181 aaatttggcgcgcagaaaatgtgttaaacagaaacacacacacatcgtaaat 240
 QY 241 ggaatgctcgttattacatttggcattactcgcgtggaagccgggtattatgc 300
 Db 241 ggaatgctcgttattacttactttagcattactaccgcgtggaagcgtgtattgc 300
 Db 301 tcacaata 308
 Db 301 tcacaata 308

RESULT 11

AD00121
 AD AAD00121 standard; DNA; 11933 BP.

AC AAD00121;

DT 31-JUL-2000 (first entry)

DE Recombinant adeno associated vector construct, PAAV-F8-1.

KM Recombinant Adeno Associated Vector; PAAV; PAAV-F8-1; human Factor VIII;
 KW hFVIII; hNF-3 albumin promoter; human elongation factor-1alpha; EF1alpha;
 KM human growth hormone; hGH; Inverted terminal repeat; ITR; haemophilia;
 KM gene therapy; ds.

OS Adeno associated virus.

PN WO200023116-A1.

PD 27-APR-2000.

PF 19-OCT-1999; 99WO-US24495.

PR 20-OCT-1998; 98US-0104994.

PR 24-MAR-1999; 99US-0125974.

PR 30-JUL-1999; 99US-0364862.

PA (AVIG-) AVIGEN INC.

TI Couto LB, Colosi PC;

DR WPI; 2000-339536/29.

XX New recombinant adenovirus-associated vector, useful for gene therapy

XX to treat hemophilia, comprises at least a portion of Factor VIII

XX operably linked to control sequence

XX Example 2; Fig 5; 92pp; English.

CC The present DNA sequence is a recombinant adenovirus-associated vector,
 CC (FAAV) construct, PAAV-F8-1. This expression vector comprises the hNF-3
 CC albumin promoter, the first intron (-573 to +985) of human elongation
 CC factor-1alpha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII)
 CC and polyadenylation signal from human growth hormone (hGH). This sequence
 CC is inserted between the AAV inverted terminal repeat (ITR) regions. The
 CC hFVIII coding region comprises the heavy chain gene segment with the
 CC first 57 bp encoding the 19 amino acid signal peptide, A1 and A2 domains
 CC and 5 amino acids from the N-terminus of the B domain. The light chain
 CC segment comprises the C-terminal 85 amino acids of B domain and the A3,
 CC C1 and C2 domains. Both the heavy and light chain segments are cloned
 CC into the same plasmid separated by 42 nucleotides coding for 14 residues
 CC of the B domain, that is deleted. This plasmid is operably linked to

CC control sequences, that directs the transcription and translation of the
 CC Factor VIII gene. The adeno-associated viral vectors are used for gene
 CC therapy to treat haemophilia. This method allows prolonged expression of
 CC therapeutic levels of Factor VIII in vivo. The FAAV are used for gene
 CC therapy, because of their broad host range, safety profile and duration
 CC of expression in the infected hosts.

XX Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;

Query Match 81.6%; Score 252; DB 21; Length 11933;

Best Local Similarity 88.6%; Pred. No. 7.5e-63;

Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atcgagataataagaatgtaaaaaatgttattcttcgcgcgtcgtgcaattattaca 60

Db 9295 atcggaataaacaacatgtgtaaaaaatgtcaccgcgtcgtcgtcgttattaca 9354

QY 61 ggaatgctcaacaaacgttactgttggaaacacacgacgagtaaccacaaagaa 120

Db 9355 ggaatgctcaacaaacgttactgttggaaacacacgacgagtaaccacaaagaa 9414

QY 121 accatcaccatcattcttcgttccggaattgacagaagaacctgtgatgagcc 180

Db 9415 accatcaccatcattcttcgttccggaattgacagaagaacctgtgatgagcc 9474

QY 181 aaatttggcgcgtgcagaaaatgtgttaaacagaaacacacacacatcgtaaat 240

Db 9475 aaatttggcgcgcagaaaatgtgttaaacagaaacacacacacatcgtaaat 9534

QY 241 ggaatgctcgttattacatttggcattactcgcgtggaagccgggtattatgc 300

Db 9535 ggaatgctcgttattactttagcattactaccgcgtggaagcgtgtattgc 9594

QY 301 tcacaata 308

Db 9595 tcacaata 9602

RESULT 12

AAD08612
 ID AAD08612 standard; DNA; 11933 BP.

AC AAD08612;

DT 04-SEP-2001 (first entry)

DE Human factor VIII expressing FAAV vector PAAV-F8-1 partial sequence.

KM Recombinant adeno-associated viral vector; FAAV; factor VIII; FVIII;
 KW blood clotting disorder; gene therapy; haemophilia A; human;
 KM PAAV-F8-1; ds.

OS Chimeric - Adeno associated virus.

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

OS Chimeric - Oryctolagus cuniculus.

PN WO200145510-A1.

PD 28-JUN-2001.

PF 21-DEC-2000; 2000WO-US34925.

PR 22-DEC-1999; 99US-0470618.

PA (AVIG-) AVIGEN INC.

TI Couto LB, Colosi PC, Qian X;

DR WPI; 2001-417955/44.

XX Treating blood clotting disorder, especially hemophilia in mammals, by

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:43:18 ; Search time 1949.42 Seconds
(without alignments)
3317.038 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 1 atgcagcataatagatgaa.....gggtatattgtccacatag 309

Sequence: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_da: 2: gb_htg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pac: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_da: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htg_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

Result No.	Query Match	Length	DB ID	Description
1	309	100.0	309	AR102880 Sequence
2	309	100.0	309	AR129424 Sequence
3	309	100.0	378	AR102879 Sequence
4	309	100.0	378	AR129423 Sequence
5	309	100.0	760	AF042279 Escherich
6	309	100.0	760	AR102863 Sequence
7	309	100.0	760	AR129407 Sequence
8	273.2	88.4	309	AR102866 Sequence
9	273.2	88.4	309	AR129410 Sequence
10	273.2	88.4	1330	X52665 E.coli DNA
11	252	81.6	309	AR102867 Sequence
12	252	81.6	309	AR129411 Sequence
13	252	81.6	326	BLANLON
14	252	81.6	9170	U02453
15	252	81.6	9205	XX002427
16	252	81.6	11313	AE005297
17	252	81.6	11933	AR138377
18	252	81.6	11933	AR146887
19	252	81.6	42539	CV039284
20	252	81.6	42530	CV039285
21	252	81.6	42531	CV039286
22	252	81.6	42704	CV037692
23	252	81.6	48502	LAMCG
24	252	81.6	61670	AF125520
25	252	81.6	65510	AP000422
26	252	81.6	327773	AP002554
27	247.2	80.0	14164	AE005330
28	247.2	80.0	16170	AE000161
29	247.2	80.0	136742	EC082598
30	247.2	80.0	222605	AP002555
31	141.6	45.8	180	AF222286
32	141.6	45.8	180	AX275633
33	141.2	45.7	752	AF441251
34	45.2	14.6	182116	AC093831
35	43	13.9	148224	AC096950
36	43	13.9	148224	AC009418
37	43	13.9	164132	AC019284
38	43	13.9	165947	AC015897
39	41	13.3	109894	AC074132
40	41	13.3	142116	AC034215
41	40.8	13.2	97451	F19K23
42	39.2	12.7	110611	AC022520
43	39.2	12.7	130235	AC008007
44	38.8	12.6	55341	AC102312
45	38.8	12.6	159981	AC069074

ALIGNMENTS

RESULT 1
LOCUS AR102880
DEFINITION Sequence 22 from patent US 6087128.
ACCESSION AR102880
VERSION AR102880.1 GI:12814468
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 309)
AUTHORS Nolan, L.K. and Horne, S.M.
TITLE DNA encoding an avian E. coli 1ss
JOURNAL Patent: US 6087128-A 22 11-JUL-2000;
FEATURES
source location/Qualifiers
1..309 /organism="unknown"
BASE COUNT 101 a 60 c 64 t 84 t
ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-68;

	Matches	309; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	1	atcgagataataagaatgaaaaaaatgttattttctgcgcctctgycgaatgcttattca	60		
Db	1	ATGCGAGATTAATAAATGAAAAAATGTTATTTCTGCGCGCTGGAATGCTTAATACA	60		
QY	61	ggatctgttcaaacaaagctttactctgttgaaacaaacgcagcgcgtaacaccaaaggaa	120		
Db	61	GGATGTGCTCAACAAACGTTTACTTTGGAAACAAACGACAGCATACACCAAAAGGA	120		
QY	121	accatcactcatcatcttctctgcttcgcggaatttgacaagagaagaaacgttatacgc	180		
Db	121	ACCATCATCATCATTTCTTCGTTCCGGGAATGGACACAGAAACCTTTATGTCAGCC	180		
QY	181	aaaatttgtcgcgctgacagaaaatgttctttaaacaagaactcagcaaacattcgtaaat	240		
Db	181	AAAAATTGTGCGCGGACGAGAAAAATGTTTAAACACAGAAACTCACCAACATTGTAAT	240		
QY	241	ggattgctccggtttatataacttttggatctctatacttcgcctggaagcccggtataatgc	300		
Db	241	GGATTGCTCGGTTTATACATTTTGGCATCTATACTCCGCTGGAGCCCGGTTATATTGC	300		
QY	301	tcacatat	309		
Db	301	TCACATATG	309		

	RESULT	2			PAT 16-MAY-2001
	LOCUS	ARI29424			
	DEFINITION	ARI29424	309 bp	DNA	
	ACCSSION	Sequence 22 from patent US 6187321.			linear
	VERSION	ARI29424			
	KEYWORDS	ARI29424..1 GI:14117321			
	SOURCE	.			
	ORGANISM	unknown.			
	REFERENCE	unclassified.			
	AUTHORS	1 (bases 1 to 309)			
	TITLE	Nojan,L.K., Horne,S.M. and Robinson,M.			
	JOURNAL	Avian E. coli iss polypeptide			
	FEATURES	Patent: US 6187321-A 22 13-FEB-2001;			
	source	Location/Qualifiers			
		1...309			
BASE COUNT	/organism="unknown"				
ORIGIN	101 a 60 c 64 g 84 t .				

Query Match	100.0%;	Score 309;	DB 6;	Length 309;
Best Local Similarity	100.0%;	Pred. NO. 2.6e-68;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Y	1	atcgaggatataaga	gtga	aaaaaaatcttattcttcgcgcgtc	gtggaatcgtctattaca	60
Oy	1	atcgaggatataaga <th>gtga</th> <th>aaaaaaatcttattcttcgcgcgtc</th> <th>gtggaatcgtctattaca</th> <th>60</th>	gtga	aaaaaaatcttattcttcgcgcgtc	gtggaatcgtctattaca	60
L+	1	ATCGAGGATTAAT	GA	GTGA	AAAAAAATGTTATTCTTCGCGCGTCTGCGAATGCTTATTACA	60
Oy	61	ggatgtgctcaaca	acgcttactcgtcttgg	aaacaacacgcagcagcagta	acaaccaaaaggaa	120
Db	61	GGATGTGCTCAACA	ACGCTTACTCGTTGG	AAACACGACGACGTAAACACCAAAAGGAA	120	
Oy	121	acctcactcatca	cttcttcgtctcgtggaa	cttgacaagaagaaacttgttga	tcagcagcc	180
Oy	121	ACCATCACTCAT	CTTCTTCGTTCCGGAA	TTGGACAAGAGAAATCGTTGATGCGACC	180	
Db	121	ACCATCACTCAT	CTTCTTCGTTCCGGAA	TTGGACAAGAGAAATCGTTGATGCGACC	180	
Oy	181	aaaatcttgtcgcg	gtgcagaaaatctgtctta	aaaacagaaactcagcaaaacttcgta	aat	240
Oy	181	AAATTTGTGCGCGT	GCAGAAAATGTTGTT	AAAACAGAAACTCAGCAAACTTGTAAT	240	
Db	181	AAATTTGTGCGCGT	GCAGAAAATGTTGTT	AAAACAGAAACTCAGCAAACTTGTAAT	240	
Oy	241	ggattgcgcggttt	tatcaactcttgg	atcatatactccgctcgtggaagcccggtatattgc	300	
Oy	241	ggattgcgcggttt	tatcaactcttgg	atcatatactccgctcgtggaagcccggtatattgc	300	
Db	241	GGATTGCGCGGTTT	TATCACTTTTGGCATCTAT	ACTCGCGCTGGAAAGCCCGGATATTATGC	300	
Oy	301	tcacagaatg	309			

Db 301 TCACATAG 309
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RESULT 3
LOCUS AR102879 378 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6087128.
ACCESSION AR102879
VERSION AR102879.1 GI:12814467
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 378)
AUTHORS Nolan,L.K. and Horne,S.M.
TITLE DNA encoding an avian E. coli iss
JOURNAL Patent: US 6087128-A 21 11-Jul-2000;
FEATURES Location/Qualifiers
source 1..378
/organism="unknown"
BASE COUNT 112 a 80 c 84 g 102 t
ORIGIN

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				Indels	0
				Gaps	0
QY	1	atgcagataataagatgaaanaaaatgtaattttctgcgcgtctgccaatgctataca	60		
Db	34	ATGCAGATAATAAGATGAANAATAATGTTATTTCTGCGCGCTCGCAATGTTATTCA	93		
QY	61	ggatgtgctcaacaagaagttactcgtttggaacaacgcagacgtaacaccaaaggaa	120		
Db	94	GGATGTGCTCAACAAGCTTTACTGTTGGAAACAACGACGACGTAAACACCAAGGAA	153		
QY	121	accatcactcatcattcttcgtttccgggaatttgaaacaagaanaaaactgtatcacgc	180		
Db	134	ACCATCACTCATCATTTCTTCGTTGCGGAATTGACACAGAANAACGTGTGATCAGCC	213		
QY	181	aaaatttggcgcgtgcagaaatgtctttaaacaagaaaactcagcaaaactcgtaaat	240		
Db	214	AAAATTGTGGCGGCGCAGAAAATGTTGTTAAACAGAAACACACCAACATTCGTAAAT	273		
QY	241	ggattgctcgcgttttatacaacttggcaactatactccgcgtggaagccgggtatattgc	300		
Db	274	GGATTGCTCGCGTTTATATCACTTTTGGCANTCTTAACCTCGCTGGAAGCCCGGTATATTGC	333		
QY	301	tcacaaatg 309			
Db	334	TCACAAATG 342			

[illegible]

Query Match 100.0%; Score 309; DB 6; Length 378;
 Best Local Similarity 100.0%; Pred. No. 2,5e-68;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcagagataaagaatgaaataatgttatttctgcgcgtctggcaatgcttattaca 60
 Db 34 ATGCAGAGATATAAGATGAAAAAATGTATTCTGCGCCCTGCGCAATGCTTATTACA 93
 QY 61 ggtatgctcaacaacagtttactgtttggaacaaacccagcaagtaaacacaaaggaa 120
 Db 94 GGATGTCCTCAACAAACGTTTACTGTGGAACAAACCGACAGCAAGTAACCAAGAA 153
 QY 121 accatcacatcatcttcttcgttcggaattggacaagaagaactgttgaagcc 180
 Db 154 ACCATCACATCATCTTCTTCGTTGCGGAATTGGACAAAGAACTGTGATGCAGCC 213
 QY 181 aaaaattgtgagcggtcagagaaatgtttaaacaagaacacagcaacattcgtaaat 240
 Db 214 AAAATTGTGCGCGTCAGAAAATGTTTAAACAGAAACTCAGCAAACTTCGTAAAT 273
 QY 241 ggtatgctcggttttacttacttcttggcatctatactccgtcggaagccgggtatattgc 300
 Db 274 GGATGTCCTCGGTTTATCACTTTGGCATCTATCTCCGCTGGAAGCCCGGTATATTGC 333
 QY 301 tcacaatag 309
 Db 334 TCACAATAG 342

RESULT 5
 AF042279 760 bp DNA linear BCT 18-SEP-2001
 LOCUS Escherichia coli 1ss (1ss) gene, complete cds.
 DEFINITION AF042279
 ACCESSION AF042279.1 GI:5305229
 VERSION AF042279.1
 KEYWORDS Escherichia coli.
 SOURCE Escherichia coli.
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

REFERENCE 1 (bases 1 to 760)
 AUTHORS Horne,S.M., Pfaff,McDonough,S.J., Giddings,C.W. and Nolan,L.K.
 TITLE Cloning and sequencing of the 1ss gene from a virulent avian Escherichia coli
 JOURNAL Avian Dis. 44 (1), 179-184 (2000)
 MEDLINE 20199920
 PUBMED 10737659
 REFERENCE 2 (bases 1 to 760)
 AUTHORS Horne,S.M., Nolan,L.K., Giddings,C.W. and Pfaff,S.J.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-1998) Vet. & Micro. Sci., North Dakota State Univ., Van Es Hall, Fargo, ND 58105, USA
 FEATURES
 source
 1..760
 /organism="Escherichia coli"
 /strain="102"
 /db_xref="taxon:562"
 /note="may be on a large R plasmid"
 292..600
 /gene="1ss"
 292..600
 /note="similar to Bacteriophage lambda Bor protein, and to 1ss protein from a septicemic human Escherichia coli isolate; causes avian colibacillosis"
 /codon_start=1
 /transl_table=11
 /product="1ss"
 /protein_id="AAD41540.1"
 /db_xref="GI:5305230"
 /translation="MODNMKKMLFSALAMLITGCAOQTFVGNKPRVATPRETITH

HEFVSGIGQKTVDAKICGGAENVKTEQTFVNGLIGTTFG
 BASE COUNT 216 a 159 c 160 g 225 t
 ORIGIN

Query Match 100.0%; Score 309; DB 1; Length 760;
 Best Local Similarity 100.0%; Pred. No. 2,5e-68;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcagagataaagaatgaaataatgttatttctgcgcgtctggcaatgcttattaca 60
 Db 292 ATGCAGAGATATAAGATGAAAAAATGTATTCTGCGCCCTGCGCAATGCTTATTACA 351
 QY 61 ggtatgctcaacaacagtttactgtttggaacaaacccagcaagtaaacacaaaggaa 120
 Db 352 GGATGTCCTCAACAAACGTTTACTGTGGAACAAACCGACAGCAAGTAACCAAGAA 411
 QY 121 accatcacatcatcttcttcgttcggaattggacaagaagaactgttgaagcc 180
 Db 412 ACCATCACATCATCTTCTTCGTTGCGGAATTGGACAAAGAACTGTGATGCAGCC 471
 QY 181 aaaaattgtgagcggtcagagaaatgtttaaacaagaacacagcaacattcgtaaat 240
 Db 472 AAAATTGTGCGCGTCAGAAAATGTTTAAACAGAACTCAGCAAACTTCGTAAAT 531
 QY 241 ggtatgctcggttttacttacttcttggcatctatactccgtcggaagccgggtatattgc 300
 Db 532 GGATGTCCTCGGTTTATCACTTTGGCATCTATCTCCGCTGGAAGCCCGGTATATTGC 591
 QY 301 tcacaatag 309
 Db 592 TCACAATAG 600

RESULT 6
 AR102863 760 bp DNA linear PAT 14-FEB-2001
 LOCUS AR102863
 DEFINITION Sequence 1 from patent US 6087128.
 ACCESSION AR102863
 VERSION AR102863.1 GI:12814451
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 760)
 AUTHORS Nolan,L.K. and Horne,S.M.
 TITLE DNA encoding an avian E. coli 1ss
 JOURNAL Patent: US 6087128-A 1 11-JUL-2000;
 FEATURES
 source
 1..760
 /organism="unknown"
 BASE COUNT 216 a 159 c 160 g 225 t
 ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 760;
 Best Local Similarity 100.0%; Pred. No. 2,5e-68;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcagagataaagaatgaaataatgttatttctgcgcgtctggcaatgcttattaca 60
 Db 292 ATGCAGAGATATAAGATGAAAAAATGTATTCTGCGCCCTGCGCAATGCTTATTACA 351
 QY 61 ggtatgctcaacaacagtttactgtttggaacaaacccagcaagtaaacacaaaggaa 120
 Db 352 GGATGTCCTCAACAAACGTTTACTGTGGAACAAACCGACAGCAAGTAACCAAGAA 411
 QY 121 accatcacatcatcttcttcgttcggaattggacaagaagaactgttgaagcc 180
 Db 412 ACCATCACATCATCTTCTTCGTTGCGGAATTGGACAAAGAACTGTGATGCAGCC 471
 QY 181 aaaaattgtgagcggtcagagaaatgtttaaacaagaacacagcaacattcgtaaat 240

RESULT	7			
LOCUS	ARI29407			
DEFINITION	ARI29407	760 bp	DNA	
ACCESSION	Sequence 1 from patent US 6187321.			linear
VERSION	ARI29407			PAT 16-MAY-2001
KEYWORDS	ARI29407.1	GI:14117304		
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified:			
AUTHORS	1 (bases 1 to 760)			
TITLE	Nolan, L.R., Horne, S.M. and Robinson, M.			
JOURNAL	Avian E. coli iss polypeptide			
FEATURES	Patent: US 6187321-A 1 13-FEB-2001;			
source	Location/Qualifiers			
	1..760			
	/organism="unknown"			
BASE COUNT	216 a	159 c	160 g	225 t
ORIGIN				

OY	1	atgcaggagtaataaataaaaaaaaaatgtattcttcgcgcctctggcaatgcttttaa	60
Dd	292	ATGCAGGATATATAGATGATAAAAAAATGTATTCTTTCGCGCCTTGCAATGCTTATTACA	351
OY	61	ggaatgtctcaacaacagcttactcgtctggaaacaacgcagcagtaacacaaagaa	120
Dd	352	GGAATGTCTCAACAACCTTTACTGTTTGAAAAACAACGACAGCTAGTAACACCAAGGAA	411
OY	121	accataactcaatcttccttcgcttcggaaattggacaagaagaataactcttatacgcc	180
b	412	ACCATCACTCATCATTTCTTGCTTCGGGAFTGGACAAGAAAACTTTATGTCAGCC	471
OY	181	aaaatctgtggcggatgcagaataatgcttctaacaagaactcagcaaacattcgtaant	240
Dd	472	AAAAATTGTGGCGGGGCAAAAAATGTTTAAAAAGAAACACACAAACATTCCTTAAT	531
OY	241	ggaatgtcgcgttttatcaactcttggcactatactccgtctgaaagcccggtatattgc	300
Dd	532	GGATTGCGCGGTTTATATCACTTTGGCATATATACTCCGCTGGAAAGCCCGGTATATTGC	591
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Dd	592	TCACAATAG 600	

[illegible]

Query Match	88.4%	Score 273.2;	DB 6,	Length 309;
Best Local Similarity	96.8%	Pred. No. 3.2e-59;		
Matches 300; Conservative	0;	Mismatches 8;	Indels 2;	Gaps 2;

Oy	1	atcgaggataataaataaaaaaaatgtattcttcgcgcgcctgggaatgcttttaa	60
Db	1	ATCGAGGATTAATAAATAAAAAAATGTTATTCTTCGCGCGCTGGCAATGCTTTACA	60
Oy	61	ggatgtgtctcaacaagaagttactctgttggaaacaacgcagcaagtaaccacaagaa	120
Db	61	GGATGTGTCTCAACAAGAGTTACTCTGTTGGAAACAACGCAGCAGTAACACCAAGAA	120
Oy	121	aacatcactcatcatcttcgtcttcggaaatctggacaagaagaaaaacgtctatgcagc	180
Db	121	ACCATCAGTCATCATCTTCTGTTCCCAATTGAGC-AGAAATAACGTGTATGCAGCC	179
Oy	181	aaaatctt-gtggcggtgagaagaatgltgtttaaacgaaactcagcaaaccttctgtaa	239
Db	180	AAAAATTGTTGGCGGTGCAGAAATGTTTAAACAGAAATCTAGCAAACTTGTGTAA	239
Oy	240	tggaattgcgtgttatacatcacttttggatcatatactccgctggaaacccggtatattg	299
Db	240	TGCATTGCCCGGTTTATCATCTTTGGCATCTATACCTCGCGGAAACCCGGTATATTG	299
Oy	300	ctcacacaatg 309	
Db	300	CTCACAAATAG 309	

[illegible]

	Query Match	Best Local Similarity	Matches	Score	DB	Length	Mismatches	Conservative	Indels	Gaps
QY	1	ATGCAGGATATATAGATGATAAAAAATGTTATTTCCTGCCGCTGCGCAATGCTTATTACA	60	88.4%	273.2	309	0	8	2	2
Db	1	ATGCAGGATATATAGATGATAAAAAATGTTATTTCCTGCCGCTGCGCAATGCTTATTACA	60	96.8%	3.2e-59	309	0	8	2	2
QY	61	GGATGTGCTCAACAACGTTTACCTGTGGAAACAACGACAGCATACACCAAGGAA	120			120				
Db	61	GGATGTGCTCAACAACGTTTACCTGTGGAAACAACGACAGCATACACCAAGGAA	120			120				
QY	121	accatcaactcatcttcttcgttcggaattcggacaagaanaactgttgatgcagcc	180			180				
Db	121	accatcaactcatcttcttcgttcggaattcggacaagaanaactgttgatgcagcc	180			180				

DB 121 ACCATCAGATCATATTTCTTCCCTCCCAATGGAC-AGAGAAAAGTGTATGACGCC 179
 OY 181 aaatttg-tggcgggtgcagaaaatgtgttaaacagaactcgcgaacttgtaaa 239
 DB 180 AAAATTGTGGCGGTGAGAAAATGTGTAAACAGAAAGTCAAGCAAACTTGTAA 239
 OY 240 tggatgcgcggtttatcaactttgcacatactccgcctggaagccgggtatgt 299
 DB 240 TGCATTGCCCGGTTTATACATTTTGGCATCTATCTCCGCGGAAACCCGTATATTG 299
 OY 300 ctcaaatag 309
 DB 300 CTCACAAATAG 309
 RESULT 10
 ECISSEGENE 1430 bp DNA linear BCT 23-JAN-1992
 LOCUS E.coli DNA for 1ss gene, a plasmid determinant coding for increased
 DEFINITION serum survival and surface exclusion.
 ACCESSION X52665
 VERSION X52665.1 GI:41843
 KEYWORDS 1ss gene.
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (bases 1 to 1430)
 AUTHORS Chude, P.J., Leon, M.A., Banerjee, A. and Palchaudhuri, S.
 TITLE Cloning and DNA sequence of plasmid determinant 1ss, coding for
 increased serum survival and surface exclusion, which has homology
 with lambda DNA
 JOURNAL Mol. Gen. Genet. 216 (2-3), 287-292 (1988)
 MEDLINE 89313666
 FEATURES
 SOURCE Location/Qualifiers
 1. 1430
 /organism="Escherichia coli"
 /db_xref="taxon:562"
 BASE COUNT 401 a 313 c 299 g 417 t
 ORIGIN

Query Match 88.4%; Score 273.2; DB 1; Length 1430;
 Best Local Similarity 96.8%; Pred. No. 2,9e-59;
 Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

OY 1 atgcagataataagaatgaataaataatgtattttctgcgcgtctgcgaatgtattaca 60
 DB 770 ATGCAGATAATAATGAATGAATAAATGTATTCTGCGGCTGCAATGCTTATTACA 829
 OY 61 ggaatgcgcgaataaagcgtttactgttgaaacaaacgcagcagtaacacaaaggaa 120
 DB 830 GGATGTGCTCAACAAACGTTTACTGTGGAACAAACCAACACCAATTAACCAAGGA 889
 OY 121 accatcacatcaattcttcgttcgggaattggaagaagaagaactgttgtagcc 180
 DB 890 ACCATCACATCATTTCTTCTGTTCCCAATGGAC-AGAGAAAAGTGTATGACGCC 948
 OY 181 aaatttg-tggcgggtgcagaaaatgtgttaaacagaactcgcgaacttgtaaa 239
 DB 949 AAAATTGTGGCGGTGAGAAAATGTGTAAACAGAAAGTCAAGCAAACTTGTAA 1008
 OY 240 tggatgcgcggtttatcaactttgcacatactccgcctggaagccgggtatgt 299
 DB 1009 TGCATTGCCCGGTTTATACATTTTGGCATCTATCTCCGCGGAAACCCGTATATTG 1068
 OY 300 ctcaaatag 309
 DB 1069 CTCACAAATAG 1078
 RESULT 11

ARI02867
 LOCUS ARI02867 309 bp DNA linear
 DEFINITION Sequence 6 from patent US 6087128.
 ACCESSION ARI02867
 VERSION ARI02867.1 GI:12814455
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 309)
 AUTHORS Nolan, L.K., Horne, S.M.
 TITLE DNA encoding an avian E. coli 1ss
 JOURNAL Patent: US 6087128-A 6 11-JUL-2000;
 FEATURES Location/Qualifiers
 source 1. 309
 /organism="unknown"
 BASE COUNT 97 a 69 c 65 g 78 t
 ORIGIN

Query Match 81.6%; Score 252; DB 6; Length 309;
 Best Local Similarity 88.6%; Pred. No. 7.6e-54;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 1 atgcagataataagaatgaataaataatgtattttctgcgcgtctgcgaatgtattaca 60
 DB 1 ATGCAGATAATAATGAATGAATAAATGTATTCTGCGGCTGCAATGCTTATTACA 60
 OY 61 ggaatgcgcgaataaagcgtttactgttgaaacaaacgcagcagtaacacaaaggaa 120
 DB 61 GGATGTGCTCAACAAACGTTTACTGTGGAACAAACCAACCAATTAACCAAGGA 120
 OY 121 accatcacatcaattcttcgttcgggaattggaagaagaagaactgttgtagcc 180
 DB 121 ACCATCACATCATTTCTTCTGTTCCCAATGGAC-AGAGAAAAGTGTATGACGCC 180
 OY 181 aaatttg-tggcgggtgcagaaaatgtgttaaacagaactcgcgaacttgtaaa 240
 DB 181 AAAATTGTGGCGGTGAGAAAATGTGTAAACAGAAAGTCAAGCAAACTTGTAA 240
 OY 241 ggaatgcgcgaataaagcgtttactgttgaaacaaacgcagcagtaacacaaaggaa 300
 DB 241 GGATGTGCTCAACAAACGTTTACTGTGGAACAAACCAACCAATTAACCAAGGA 300
 OY 301 tcaaatag 308
 DB 301 TCACAAATAG 308
 RESULT 12

ARI29411
 LOCUS ARI29411 309 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 6 from patent US 6187321.
 ACCESSION ARI29411
 VERSION ARI29411.1 GI:14117308
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 309)
 AUTHORS Nolan, L.K., Horne, S.M. and Robinson, M.
 TITLE Avian E. coli 1ss polypeptide
 JOURNAL Patent: US 6187321-A 6 13-FEB-2001;
 FEATURES Location/Qualifiers
 source 1. 309
 /organism="unknown"
 BASE COUNT 97 a 69 c 65 g 78 t
 ORIGIN

Query Match 81.6%; Score 252; DB 6; Length 309;
 Best Local Similarity 88.6%; Pred. No. 7.6e-54;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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OY 1 atcgagataaataaataaataatcttctgcgcgtctggcaatgctattaca 60
DB 1 ATCGGGAATTAACACCAATAAATAATGCTACTGCGCTAGCGCCCTGTTATTACA 60
OY 61 ggaatgtctcaacaacagttactctgttgaataaaccgacagcgttaaccacaaaggaa 120
DB 61 GGATGTGCTCAACAGACGCTTACTGTTTAAACAAACCGCGCAGCGAGTACACCAAGAA 120
OY 121 accatcatcatcttcttctgcgttctgggaattggacaagaagaactggttgcacgc 180
DB 121 ACCATCACCAATCATTTCTTCTGCTTCTGGAATGGCGAAGAAACTGTGCATGACGCC 180
OY 181 aaatttggcgcgtgacgaataatgtttaaacaagaactcagcaaacattcgttaaat 240
DB 181 AAAATTTGTGGCGCGCGAGAAAATGTGTAAACAGAAACCCAGCAACATTCCTAAAT 240
OY 241 ggaatgtcgcgtttattactcttggcactatactcgcgcgtggaagcccggtatattgc 300
DB 241 GGATGTGCTCAACAGACGCTTACTGTTTAAACAGAAACCCAGCAACATTCCTAAAT 300
OY 301 tcacata 308
DB 301 TCACATA 308
OY 301 tcacata 308
DB 301 TCACATA 308

RESULT 13
BLANLON
LOCUS Bacteriophage lambda bor gene. 326 bp DNA Linear PHG 04-MAR-1994
DEFINITION X55792
VERSION X55792.1 GI:288763
KEYWORDS envelope protein.
SOURCE bacteriophage lambda.
ORGANISM bacteriophage lambda.
VIRUSES: dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
lambda phage group.
REFERENCE 1 (bases 1 to 326)
AUTHORS Barondess,J.J. and Beckwith,J.
TITLE A bacterial virulence determinant encoded by lysogenic coliphage
lambda
JOURNAL Nature 346 (6287), 871-874 (1990)
MEDLINE 90363299
FEATURES
SOURCE Location/Qualifiers
1..326
/organism="bacteriophage lambda"
/db_xref="taxon:10710"
24..317
/gene="bor"
24..317
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24..317
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/transl="MKMLATLALITGCAOQFTVONKPAVAVKERTTHFFVS
GIGOKKVDAAKICGGAENVKETOQTFVNGILGFTLGIYPLEARVYCSQ"
BASE COUNT 104 a 72 c 69 g 81 t
ORIGIN
Query Match 81.6%; Score 252; DB 7; Length 326;
Best Local Similarity 88.6%; Pred. No. 7.6e-54;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
OY 1 atcgagataaataaataaataatcttctgcgcgtctggcaatgctattaca 60
DB 1 ATCGGGAATTAACACCAATAAATAATGCTACTGCGCTAGCGCCCTGTTATTACA 68
OY 61 ggaatgtctcaacaacagttactctgttgaataaaccgacagcgttaaccacaaaggaa 120
DB 61 GGATGTGCTCAACAGACGCTTACTGTTTAAACAAACCGCGCAGCGAGTACACCAAGAA 128
DB 69 GGAATGTGCTCAACAGACGCTTACTGTTTAAACAAACCGCGCAGCGAGTACACCAAGAA 128

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OY 121 accatcatcatcttcttctgcgttctgggaattggacaagaagaactggttgcacgc 180
DB 129 ACCATCACCAATCATTTCTTCTGCTTCTGGAATGGCGAAGAAACTGTGCATGACGCC 188
OY 181 aaatttggcgcgtgacgaataatgtttaaacaagaactcagcaaacattcgttaaat 240
DB 189 AAAATTTGTGGCGCGCGAGAAAATGTGTAAACAGAAACCCAGCAACATTCCTAAAT 248
OY 241 ggaatgtcgcgtttattactcttggcactatactcgcgcgtggaagcccggtatattgc 300
DB 249 GGATGTGCTCAACAGACGCTTACTGTTTAAACAGAAACCCAGCAACATTCCTAAAT 308
OY 301 tcacata 308
DB 309 TCACATA 316

RESULT 14
LOCUS 9170 bp DNA Linear SYN 29-MAR-1996
DEFINITION Cloning vector lambda EMBL3, right arm.
ACCESSION U02453
VERSION U02453.1 GI:413819
KEYWORDS Cloning vector lambda EMBL3.
SOURCE Cloning vector lambda EMBL3.
ORGANISM Cloning vector lambda EMBL3.
REFERENCE 1 (bases 1 to 9170)
AUTHORS Kitz,P.A.
TITLE ClonTECH Vectors On Disc version 1.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9170)
AUTHORS Frischauf,A.M., Lehrach,H., Poustka,A. and Murray,N.
TITLE lambda replacement vectors carrying polylinker sequences
JOURNAL J. Mol. Biol. 170 (4), 827-842 (1983)
MEDLINE 84064856
REFERENCE 3 (bases 1 to 9170)
AUTHORS Kitz,P.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1993) Paul A. Kitz, CLONTECH Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT This sequence has been compiled from information in the sequence
databases, published literature and other sources. If you suspect
there is an error in this sequence, please contact CLONTECH's
Technical Service Department at (415) 424-8222 or (800) 662-2566,
extension 3 or E-mail TECH@CLONTECH.COM.
FEATURES
SOURCE Location/Qualifiers
1..9170
/organism="Cloning vector lambda EMBL3"
/db_xref="taxon:31783"
BASE COUNT 2534 a 1996 c 2251 g 2389 t
ORIGIN
Query Match 81.6%; Score 252; DB 12; Length 9170;
Best Local Similarity 88.6%; Pred. No. 6.4e-54;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
OY 1 atcgagataaataaataaataatcttctgcgcgtctggcaatgctattaca 60
DB 7435 ATCGGGAATTAACACCAATAAATAATGCTACTGCGCTAGCGCCCTGTTATTACA 7376
OY 61 ggaatgtctcaacaacagttactctgttgaataaaccgacagcgttaaccacaaaggaa 120
DB 7375 GGATGTGCTCAACAGACGCTTACTGTTTAAACAAACCGCGCAGCGAGTACACCAAGAA 7316
OY 121 accatcatcatcttcttctgcgttctgggaattggacaagaagaactggttgcacgc 180
DB 7315 ACCATCACCAATCATTTCTTCTGCTTCTGGAATGGCGAAGAAACTGTGCATGACGCC 7256
OY 181 aaatttggcgcgtgacgaataatgtttaaacaagaactcagcaaacattcgttaaat 240
DB 181 AAAATTTGTGGCGCGCGAGAAAATGTGTAAACAGAAACCCAGCAACATTCCTAAAT 240

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Wed Jul 24 10:09:05 2002

us-09-738-599-22.rge

Search completed: July 23, 2002, 13:43:20
Job time: 7471 sec

Db 7255 AAAATTGTCGGCGCCAGAAAATGTTGTAACAGAAACCAGCAACATTCGTAAAT 7196
QY 241 ggaatgcgcgtttatcatttgcatttgcatttgcatttgcatttgcatttgc 300
Db 7195 GGATGCTCGCTTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 7136
QY 301 tcacacata 308
Db 7135 TCACACATA 7128

RESULT 15
XXU02427/c 9205 bp DNA linear SYN 29-JAN-1997
LOCUS Cloning vector lambda EMBL3 SP6/T7, right arm.
DEFINITION U02427
VERSION U02427.1 GI:413793
KEYWORDS Cloning vector lambda EMBL3 SP6/T7.
SOURCE Cloning vector lambda EMBL3 SP6/T7
ORGANISM artificial sequence; vectors.
REFERENCE 1 (bases 1 to 9205)
Kilts, P.A.
Clontech Vectors On Disc version 1.3
Unpublished
Kilts, P.A.
2 (bases 1 to 9205)
Clontech Vectors On Disc version 1.3
Unpublished
Kilts, P.A.

REFERENCE AUTHORS
TITLE Clontech Vectors On Disc version 1.3
JOURNAL Unpublished
AUTHORS Kilts, P.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1993) Paul A. Kilts, Clontech Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
AUTHORS This sequence has been compiled from information in the sequence
JOURNAL databases, published literature and other sources. If you suspect
there is an error in this sequence, please contact Clontech's
Technical Service Department at (415) 424-8222 or (800) 662-2566,
extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES
source 1. 9205
location/Qualifiers
/organism="Cloning vector lambda EMBL3 SP6/T7"
/db_xref="taxon:31784"
BASE COUNT 2546 a 2002 c 2253 g 2404 t
ORIGIN

Query Match 81.6%; Score 252; DB 12; Length 9205;
Best Local Similarity 88.6%; Pred. No. 6.4e-54;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atgcaggtatataagataaataatgttattcttcgcgcgtctggaatgctattaca 60
Db 7470 ATCGGGAAATACACCAATGAAAAAATGCTACTGCGCTGCGCTGCTTATTACA 7411
QY 61 ggaatgctcaacaacgttactgttgaacaacacgacagcaagtaaccacaagaa 120
Db 7410 GGATGCTCGCTTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 7351
QY 121 accatcaccatcattcttcgttcggaattgacagaagaagaacgttgaatgaccc 180
Db 7350 ACCATCACCACATCTTCTGCTTCTGGAATGGCAGAGAGAAAACCTGCGATGCAGCC 7291
QY 181 aaaaattgaggcggtgcagaaaatgttgaagaagaacacacgaacacatcgttaaat 240
Db 7290 AAAATTGTCGGCGCCAGAAAATGTTGTAACAGAAACCAGCAACATTCGTAAAT 7231
QY 241 ggaatgctcggtttatcatttgcatttgcatttgcatttgcatttgcatttgc 300
Db 7230 GGATGCTCGCTTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 7171
QY 301 tcacacata 308
Db 7170 TCACACATA 7163

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:04:54 ; Search time 2538.62 Seconds
(without alignments)
2009.694 Million cell updates/sec

Title: US-09-738-599-21

Perfect score: 378

Sequence: 1 cctgaagctctgtccagcagc.....ggagctcattcgcgaattcc 378

Scoring table: IDENTIFY_NTC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estbta:*
2: em_estbta:*
3: em_estbta:*
4: em_estbta:*
5: em_estbta:*
6: em_estbta:*
7: em_estbta:*
8: em_estbta:*
9: gb_estbta:*
10: gb_estbta:*
11: gb_estbta:*
12: gb_estbta:*
13: em_gss_hum:*
14: em_gss_hum:*
15: em_gss_hum:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	232	61.4	332	9	AM619529 7594 MARC
2	187.2	49.5	731	9	AV398499 AV398499
3	143.8	38.0	240	9	AM659631 97104 MAR
4	139.8	37.0	785	9	A1547008
5	123.8	32.8	223	10	C22108
6	120.6	31.9	160	10	BG895793
7	119	31.5	160	10	BG835172
8	109.6	29.0	162	10	B138974
9	109.4	28.9	336	10	BE51841
10	89.4	23.7	178	10	B142815
11	65.8	17.4	802	9	A1546999
12	63.2	16.7	594	10	BE493915
13	45.4	12.0	299	9	AA547917
14	45.2	12.0	560	12	B84811
15	45.2	12.0	634	12	AQ309897
16	42.8	11.3	532	12	AQ344521
17	38.8	10.3	733	12	A2131766

18	38.8	10.3	914	12	A2539756
19	38.6	10.2	426	9	AV532310
20	38.6	10.2	599	9	AV537481
21	38.4	10.2	520	12	A2927608
22	38	10.1	514	10	BM168198
23	37.4	9.9	183	12	B88032
24	37.4	9.9	524	12	A2525395
25	37.4	9.8	488	12	AG024048
26	37.2	9.8	404	12	CNS02048
27	37.2	9.8	404	10	B1514353
28	37	9.8	458	10	B1510802
29	37	9.8	559	10	B1510865
30	36.8	9.7	478	9	AM288591
31	36.8	9.7	582	12	AQ629690
32	36.8	9.7	681	12	A2522631
33	36.8	9.7	681	10	BE658070
34	36.4	9.6	733	10	BF680474
35	36.2	9.6	500	9	A0086381
36	36	9.5	617	12	A2856405
37	36	9.5	713	12	BH029375
38	36	9.5	1101	12	CNS01610
39	35.8	9.5	494	10	B1745078
40	35.8	9.5	496	9	AA842275
41	35.6	9.4	885	12	CNS013ET
42	35.4	9.4	771	9	AL516158
43	35.4	9.4	1101	12	CNS05RM7
44	35.2	9.3	392	10	BM258478
45	35.2	9.3	468	9	AV618307

ALIGNMENTS

RESULT 1
LOCUS AM619529/c 332 bp mRNA linear EST 24-MAR-2000
DEFINITION 7594 MARC PBE Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AM619529
VERSION AM619529.1 GI:7325713
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE Smith,T.P.L., Fahrenkrug,S.C., Rohrer,G.A., Slommen,F.A., Rexroad
1 (bases 1 to 332)
C.D.N.A. library
CDNA library
Anim. Genet. 32 (2), 66-72 (2001)
21314990
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross-match with the -mlnsc018
and -mlnmatch 12 options.
PCR Primers
FORWARD: GGAACAGCTATGACCATG
BACKWARD: GTAAACGAGCGGACGT
Seq primer: AATTAACCTCTACCTAAGCG.
Location/Qualifiers
1. 332
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC_PBE"
/issue_type="Day 12 whole embryos"
/lab_host="X10LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Library made from pool of embryos in spherical and

FEATURES
source

ORIGIN

BASE COUNT ORIGIN	10 a	51 c	54 g	6 / e
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Query Match	38.08;	Score 143.8;	DB 9;	Length 240;
Best Local Similarity	90.18;	Pred. No. 5.6e-30;		

	Matches	154,	Conservative	0;	Mismatches	17;	Indels	0;	Gaps	0;
QY	176	tttcgggaattgagacaagagaactgttgaatgcagccaaatattgtgcygtgcagaa	235							
Db	240	ttttctgggaattggcgacagaagaaactgttcgaatgcagccaaattttgtggcgcgagaa	181							
QY	236	atgtgttcaaaacagaactcagcaaacattgttaatggatgtgcgtttatcaact	295							
Db	180	atgtgtttttaaacaacaaacccaccaaaccttgcgttaattgattgcgtttttattactt	121							
QY	236	tttcgacatcatactcgcctggaagcccggtatattgtcacaatagttgc	346							
Db	120	taggcattttattactccctcgaaagcgcgctgtattgtccccaattattgc	70							

FEATURES	SOURCE
Location/Qualifiers	1. .785
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/db_xref="taxon:9606"	
/clone_lib="mynorm"	
cdata="Organ: Prostate; Vector: pBluescript; Directional	
cdna library was constructed using Lambda Zp II Kit	
(Stratagene). mRNA was extracted from a frozen normal	
prostate tissue (Mayo Clinic)."	
BASE COUNT	153 a 128 c 147 g 229 t 128 others
ORIGIN	

Query Match	37.0%	Score 139.8	DB 9	Length 785
Best Local Similarity	78.0%	Pred. No. 9.5e-29		
Matches 199	Conservative 0	Mismatches 52	Indels 4	Gaps 3

QY	42	taataagattgaaaaaatagtattttctgcgcgtcttgcaatgctattacagatgtgc	101
Db	255	TAATAGAGCTNCNTATNAGGCNAAATTTGTATGCCGNCOCCTCTANTACGGAGAGNTC	196
QY	102	--tcacaacaagctttactcgttgaaac--aaacgcacagcagtaacaaccaaaggaaac--a	157
Db	195	CACCAAGACAGGTTTACAGGTCATAAACAACCGGACAGCAGTAGACCAACCAAGAAACCA	136
QY	158	tcaatcatcatcttcttcggttcgcggaatttgcagaagaagaacvtctgtcagcccaaa	217
Db	135	TCACCCACATCTTCTCTCTTGAAATTTGGCCACAAGAAACCTGCTGATGAGCCAAAA	76
QY	218	ttctgagcgcgtgcagaagaatgtgttaaacacagaacctcagcaaacatttcgtaaatgcat	277
Db	75	TTTGTGGGGGGGCAGAAATGTGTGTTAATAACGAACCCAGCAAACTTCGTGTAANANGAT	16

					Email: om9330@okt.afric.go.jp
					PROJECT - Citrus Genome Analysis.
FEATURES					Location/Qualifiers
SOURCE					1..223
					/organism="Citrus unshiu"
					/strain="Miyagawa-wase satsuma mandarin"
					/db_xref="taxon:51188"
					/clone="pcMR1719.66"
					/clone_1lb="Miyagawa-wase satsuma mandarin orange (M.Omura)
)
					/tissue_type="juice sac and pulp segment"
					/dev_stage="rapid developing stage"
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Best Local Similarity					80.5%; Pred. No.2.3e-24;
Matches 157; Conservative					0; Mismatches 37; Indels 1; Gaps 1;
Oy	39	ggaataagaatgaaataaatgttatcttcctgcgcgtcttgcaatcgtattacagagt	98		
Db	13	GAAATACGCCATGAAAAAATCTCCTACTGCCTACTGGCTTGTCCCGCTTTATTACAGAGT	72		
Oy	99	tggccaagaacaagttactgttgtggaacaacaaccgcacacgtaaaaaccaaaggaaaccat	158		
Db	73	TGCTAACAGACGTTACTTCATTGTCANAAACAACCAGCACAGTAGCAACCAAGAAACCAT	132		
Oy	159	cactcatcattcttcgittcggttcgysgaatgyacaagaagaanaactgttgaatgcagccaaat	218		
Db	133	CACCATCATTTCTTCGTTTCYGAAATTGGGC-AGAGA AACCTGTGTGCACCCAAATAAT	191		
Oy	219	ttgttgcggtgcagaa	233		
Db	192	TTTGCGCGAGAGAAA	206		
RESULT	6				
BG895793/c					
LOCUS	BG895793				160 bp mRNA linear EST 05-JUN-2001
DEFINITION	358430 MARC IPig Sus scrofa CDNA 5', mRNA sequence.				
ACCESSION	BG895793				
VERSION	BG895793.1				GI:14306034
KEYWORDS	EST.				

SOURCE
ORGANISM pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE
AUTHORS 1 (bases 1 to 160)
Fahrenkrug, S.C., Fekling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACATCGACGAG
Plate: 123 row: L column: 23
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Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_id="MARC 1Pig"
/tissue_type="Pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 46 a 37 c 31 g 46 t
ORIGIN

Query Match 31.9%; Score 120.6; DB 10; Length 160;
Best Local Similarity 93.3%; Pred. No. 1.7e-23;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 212 ccaaaattgtgctgaggaataatgtttaaacaagaactcgaacattcgtaa 271
DB 160 CCAAAATTGTGCTGCGCGCGAGAAAATGTGTTAAACAGAAACCCAGCAACTTCGTAA 101

QY 272 atgagattgtcgtgtttatcacttttgacatctatactccgctggaagccgggtatatt 331
DB 100 ATGAGATTGCTCGGTTTATTACTTTAGCATTTATATCTCCGCTGGAAGCGCTGTATT 41

QY 332 gctcacataagttgc 346
DB 40 GCTCACATAATATTGC 26

RESULT 7
BG835172/c 160 bp mRNA linear EST 25-MAY-2001
LOCUS 353618 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
DEFINITION BG835172
ACCESSION BG835172.1 GI:14201080
VERSION
KEYWORDS EST.
SOURCE
ORGANISM pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE
AUTHORS 1 (bases 1 to 160)
Fahrenkrug, S.C., Fekling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACATCGACGAG
Plate: 116 row: L column: 23
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_id="MARC 1Pig"
/tissue_type="Pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 47 a 37 c 31 g 45 t
ORIGIN

Query Match 31.5%; Score 119; DB 10; Length 160;
Best Local Similarity 92.6%; Pred. No. 4.9e-23;
Matches 125; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 212 ccaaaattgtgctgaggaataatgtttaaacaagaactcgaacattcgtaa 271
DB 160 CCAAAATTGTGCTGCGCGCGAGAAAATGTGTTAAACAGAAACCCAGCAACTTCGTAA 101

QY 272 atgagattgtcgtgtttatcacttttgacatctatactccgctggaagccgggtatatt 331
DB 100 ATGAGATTGCTCGGTTTATTACTTTAGCATTTATATCTCCGCTGGAAGCGCTGTATT 41

QY 332 gctcacataagttgc 346
DB 40 GCTCACATAATATTGC 26

RESULT 8
BI338974/c 162 bp mRNA linear EST 30-JUL-2001
LOCUS 363710 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
DEFINITION BI338974
ACCESSION BI338974
VERSION BI338974.1 GI:15032257
KEYWORDS EST.
SOURCE
ORGANISM pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE
AUTHORS 1 (bases 1 to 162)
Fahrenkrug, S.C., Fekling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.

BASE COUNT	46 a	34 c	40 g	58 t
ORIGIN				
Query Match	23.7%	Score 89.4	DB 10	Length 178
Best Local Similarity	82.9%	Pred. No. 1.1e-14		
Matches 102	Conservative 0	Mismatches 21	Indels 0	Gaps 0
QY	33	catgcagagataataagatgtaaaaaaatgtctatttctgcgcgtcttgcaatgtctattac	92	
DB	123	CATGGGAAATACACATGAAAAAAATCTACTGCTACTGCTGCGTGGCCCTGCTAATAC	64	
QY	93	aggatgtctcaacaacagttactgttggtaaaacacgcagcagtaaacaccaaagga	152	
DB	63	AGGATGTGCTCAACAGACGTTACTGTTCAAAACAAACCGGACACAGTAGACACCAAGA	4	
-QY	153	aac 155		
DB	3	AAC 1		
RESULT 11				
DEFINITION	A1546999	802 bp	mRNA	linear
LOCUS	PN.1.12.G12.r	mynorm	Homo sapiens	CDNA 5', mRNA sequence.
ACCESSION	A1546999			
VERSION	A1546999.1	GI:4464487		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 802)			
AUTHORS	Huang, G.M., Ng, W.L., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J., and Hood, L.			
TITLE	Prostate cancer expression profiling by cDNA sequencing analysis			
JOURNAL	Genomics 59 (2), 178-186 (1999)			
MEDLINE	99393982			
COMMENT	Contact: Guyang Matthew Huang Leroy Hood University of Washington Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195 Tel: 5106280100 Fax: 5106280108 Email: huanggm@yahoo.com.			
FEATURES	Location/Qualifiers			
source	1..802			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone.lib="mynorm"			
	/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a frozen normal prostate tissue (Mayo Clinic)." 125 others			
BASE COUNT	179 a	152 c	163 g	183 t
ORIGIN				
Query Match	17.4%	Score 65.8	DB 9	Length 802
Best Local Similarity	88.6%	Pred. No. 6.2e-08		
Matches 70	Conservative 0	Mismatches 9	Indels 0	Gaps 0
QY	151	gaacacatacacaataattcttcgttgcggagatggacaagagaaaactgttgatga	210	
DB	1	GAACACATACCCATCATTTCTTCGTTCTGGAATGGCGCAAGAAAACACTGCGATGCA	60	
QY	211	gccaaaattgttggcggctg	229	
DB	61	GCCAAAATTGTGGCGCG	79	
RESULT 12				

FEATURES	BE493915	LOCUS	594 bp	MRNA	linear	EST 02-AUG-2000
DEFINITION	WHE1276_B06.C12S	Secale cereale	another cDNA library	Secale cereale		
ACCESSION	BE493915					
VERSION	BE493915.1	GI:9660508				
KEYWORDS	EST.					
SOURCE	rye.					
ORGANISM	Secale cereale					
REFERENCE	Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.					
AUTHORS	The structure and function of the expressed portion of the wheat genomes - Another cDNA library from rye					
TITLE	Unpublished (2000)					
JOURNAL	Contact: Olin Anderson					
COMMENT	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center					
	800 Buchanan Street, Albany, CA 94710, USA					
	Tel: 5105955773					
	Fax: 5105938618					
	Email: oanderson@wv.usda.gov					
	Sequence has been trimmed to remove vector sequence and low quality sequence with phred score less than 20					
	Seq primer: Stragene SK primer.					
	Location/Qualifiers					

FEATURES	SOURCE	Location/Qualifiers
		1. 594
		/organism="Secale cereale"
		/cultivar="Blanco"
		/db_xref="taxon:4550"
		/clone="WHE1276_B06_C12"
		/clone_id="Secale cereale anther cDNA library"
		/tissue_type="Anther"
		/dev_stage="Adult plant before anthesis"
		/lab_host="E. coli SOLR"
		/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early melosis to late melosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give phuescript phagmids in the TV close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT	136 a 150 c 142 g 166 t	
ORIGIN		
Query Match	16.7% Score 63.2 DB 10 Length 594;	
Best Local Similarity	89.5% Pident NO.3.2e-076	
Matches 68; Conservative	0; Mismatches 8; Indels 0; Gaps 0;	
QY 271 aatgagatgctcggtttacacttttgcacatcactcgcgtggaagccgggtatcat 330		
DB 17 AAAGGATTCCTCGGTTTATCTTACCTTAGGCATTATCTCCGCGTGAAGCGCGTGTGTAT 76		
QY 331 tgcctacatagttgc 346		
DB 77 TGCCTCACATTAATGCG 92		
RESULT 13		
AA547917/c		
LOCUS	299 bp mRNA linear EST 22-SEP-1997	
DEFINITION	MB3D6V2G05T3 Brugia malayi day 6 post-infection third stage larvae	
	SAW66MLM-fml3d6 Brugia malayi cDNA clone 3D6V2G05 5', mRNA	
	sequence.	

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 634)
Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Sub, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.

TITLE

Use of a random human BAC End Sequence Database for Sequence-Ready

JOURNAL
COMMENT

Map Building
Unpublished (1998)
Other GSSs: CITBI-EL-2522C23.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..634.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2522C23"
/clone_11b="CITBI-EL"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT
ORIGIN

274 a 123 c 89 g 148 t

Query Match

12.0%; Score 45.2; DB 12; Length 634;

Best Local Similarity 48.8%; Pred. No. 0.037;
Matches 122; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

```

QY 41 ataataagatgaaaaaatgtattttctgcgcgtctgcaatgtctattacagatgtg 100
   || || || || || || || || || || || || || || || || || || || ||
Db 309 ATTGACACAGACAGAGATGCTTCTTCTACTCCATCCACATGACTAGAAAGTG 368
   || || || || || || || || || || || || || || || || || || ||
QY 101 ctcaacaagcttactctgttgaaacaacagcagcagtaaccacaaaggaaaccatca 160
   || || || || || || || || || || || || || || || || || || ||
Db 369 CTAGCCAGACAAATCAGGTATGATTAATCAAAAGCGTCAAAACAAAAGAAAGTCAAAA 428
   || || || || || || || || || || || || || || || || || || ||
QY 161 ctcatcattctcgttcgggaattggacaagaagaacgtgtgatgcagccaaattt 220
   || || || || || || || || || || || || || || || || || || ||
Db 429 TATCTCTCATCATGATATATAAATTCTATCTAGAGAACCTGAGACACCAACCAAGA 488
   || || || || || || || || || || || || || || || || || || ||
QY 221 gtgcgcgtgcgaagaatgtcttaaaacagaacactcagaacacatcgtaaatgattgc 280
   || || || || || || || || || || || || || || || || || || ||
Db 489 CTCTGTGACTGATGATATGTCAGTAAAGTTTCAGATACAAATAAGTGTACAAAATATAG 548
   || || || || || || || || || || || || || || || || || || ||
QY 281 tcggtttat 290
   || || || || || || || || || || || || || || || || || || ||
Db 549 TAGCATTTT 558
   || || || || || || || || || || || || || || || || || || ||

```

Search completed: July 23, 2002, 13:10:30
Job time: 7536 sec

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94364 represent novel human diagnostic coding sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

	RESULT	15
AAAA26702		
ID	AAAA26702	standard; cDNA; 1685 BP.
XX		
AC	AAAA26702;	
XX		
DT	23-JUN-2000	(first entry)
XX		
DE	Candida albicans polynucleotide sequence #40.	
XX		
XX		
KM	Candida albicans infection; growth; survival; medicament; AIDS	
KX	vulvovaginitis; immunocompromised patient; treat; ss.	

This sequence represents a polynucleotide sequence encoding a polypeptide that is critical for the survival and growth of *Candida albicans*. The C. *albicans* nucleic acid molecules of the invention may be used as probes and primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C. *albicans* associated diseases, especially in AIDS patients and to treat vulvovaginitis in otherwise healthy females. The use of the polypeptides and polynucleotide sequences to treat C. *albicans* associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for immunocompromised patients, such as AIDS patients.

Sequence 1685 BP; 650 A; 281 C; 250 G; 504 T; 0 other;

Search completed: July 23, 2002, 13:51:26
Job time: 5377 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 12:19:59 ; Search time 99.46 Seconds

(Without alignments)
933.536 Million cell updates/sec

Title: US-09-738-599-21

Perfect score: 378
Sequence: 1 ctggaagtccttcctccagg.....ggagctcattcgcattcc 378Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, NA:*

- 1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
- 3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
- 6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	100.0	378	3	US-09-023-221A-21
2	378	100.0	378	4	US-09-282-352A-21
3	339.8	89.9	760	3	US-09-023-221A-1
4	339.8	89.9	760	4	US-09-282-352A-1
5	309	81.7	309	3	US-09-023-221A-22
6	309	81.7	309	4	US-09-282-352A-22
7	273.2	72.3	309	3	US-09-023-221A-5
8	273.2	72.3	309	4	US-09-282-352A-5
9	256.4	67.8	11933	4	US-09-470-618-13
10	256.4	67.8	11933	4	US-09-364-862-13
11	252	66.7	309	3	US-09-023-221A-6
12	252	66.7	309	4	US-09-282-352A-6
13	34.2	9.0	1519	4	US-09-002-361-4
14	33.6	8.9	1817	2	US-08-743-637B-1
15	33.6	8.9	1817	3	US-08-526-840B-1
16	32.8	8.7	4380	1	US-07-582-945-1
17	32.8	8.7	4380	2	US-08-453-141-1
18	32.8	8.7	4380	3	US-08-293-314-1
19	32.4	8.6	1925	2	US-08-553-436A-1
20	32.2	8.5	408	4	US-09-328-111-169
21	32.2	8.5	1690	1	US-08-276-452A-24
22	32.2	8.5	1690	2	US-08-798-744-24
23	31.2	8.3	90050	4	US-09-245-041-5
24	30.6	8.1	1504	2	US-08-878-989-10
25	30.6	8.1	1504	4	US-09-272-796-10
26	30.6	8.1	1576	2	US-09-197-378-1
27	30.2	8.0	2089	1	US-08-552-142A-1

28	30.2	8.0	2089	1	US-08-910-973-1	Sequence 1, Appl
29	30.2	8.0	2089	5	PCT-US95-05741-1	Sequence 1, Appl
30	30	7.9	34	3	US-09-023-221A-11	Sequence 11, Appl
31	30	7.9	34	4	US-09-282-352A-11	Sequence 11, Appl
32	29.8	7.9	2431	3	US-08-714-918-15	Sequence 15, Appl
33	29.8	7.9	2431	4	US-09-265-315-15	Sequence 15, Appl
34	29.8	7.9	2431	4	US-09-265-315-15	Sequence 15, Appl
35	29.8	7.9	2431	4	US-09-265-315-15	Sequence 15, Appl
36	29.8	7.9	2943	2	US-08-788-892-1	Sequence 1, Appl
37	29.6	7.8	2525	3	US-08-714-918-84	Sequence 84, Appl
38	29.6	7.8	2525	4	US-09-265-315-84	Sequence 84, Appl
39	29.6	7.8	2525	4	US-09-265-315-84	Sequence 84, Appl
40	29.6	7.8	2525	4	US-09-265-315-84	Sequence 84, Appl
41	29.6	7.8	3825	3	US-08-904-263A-3	Sequence 3, Appl
42	29.4	7.8	237	3	US-08-904-263A-5	Sequence 5, Appl
43	29.4	7.8	421	4	US-08-976-259-92	Sequence 92, Appl
44	29.4	7.8	846	2	US-08-743-637B-189	Sequence 189, App
45	29.2	7.7	595	4	US-09-385-982-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-023-221A-21
Sequence 21, Application US/09023221A
Patent No. 6087128
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023, 221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-21

Query Match: 100.0%; Score 378; DB 3; Length 378;
Best Local Similarity: 100.0%; Pred. No. 3.2e-112;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctggaagtccttcctccaggcccttggtatcgcaggaataaagatgaataatg 60
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DB 1 ctggaagtccttcctccaggcccttggtatcgcaggaataaagatgaataatg 60
|||||

QY 61 ttatttcgcgcctcgtgcaatgcttattacagagatgctcaacaacgcttactgtt 120
|||||
Db 61 TATTITTCGCCGCTTGCAATGCTTATTACAGATGTCCTCAACAAACGTTACTGTT 120
QY 121 ggaacaaacgcagcagtaaacacaaaggaaacatactcaatcattcttcgcttcg 180
|||||
Db 121 GGAACAAACGCAGCAGTAAACACCAAGAAACCATCATCATCTTCTTCGTTGCG 180
QY 181 ggaattggacaagagaacactgttgatgacgcaaaatttggcggtgcagaanaatgtt 240
|||||
Db 181 GGAATTGGACAAGAGAAACTGTGTATGACGCAAAATTTGGCGGTGCAGAAATGTT 240
QY 241 gttaaacagaacactcaagaacattcgttaattgattgctcggttttcaactttggc 300
|||||
Db 241 GTTAAACAGAAACTCAGCAAACTTCGTAATGATGCTCGTTTATCACTTTTGGC 300
QY 301 atctatactcgcctggaagcccggtatattgctcacaaatgcttgcacatgataatg 360
|||||
Db 301 ATCTATACTCCGCTGGAAGCCCGGGTATATGCTCACAATAGTTGCCCATATGATGGG 360
QY 361 agctatctcgcgaattcc 378
|||||
Db 361 AGCTCATCTGCGAATTC 378

RESULT 2

US-09-282-352A-21
Sequence 21, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: ROBINSON, SHELEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282.352A
FILING DATE: 31-MAR-1999

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023.221
FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-282-352A-21

Query Match 100.0%; Score 378; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 3.2e-112;

Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctggaagttcttctcgaagggccctcggtatccatgcaagataaataagataaag 60
|||||
Db 1 CTGGAAGTTCTCTTCAGGGGCCCTCGGTATCCATGCAAGATAAATGAATGAAAAAATG 60
QY 61 ttatttcgcgcctcgtgcaatgcttattacagagatgctcaacaacgcttactgtt 120
|||||
Db 61 TATTITTCGCCGCTTGCAATGCTTATTACAGATGTCCTCAACAAACGTTACTGTT 120
QY 121 ggaacaaacgcagcagtaaacacaaaggaaacatactcaatcattcttcgcttcg 180
|||||
Db 121 GGAACAAACGCAGCAGTAAACACCAAGAAACCATCATCATCTTCTTCGTTGCG 180
QY 181 ggaattggacaagagaacactgttgatgacgcaaaatttggcggtgcagaanaatgtt 240
|||||
Db 181 GGAATTGGACAAGAGAAACTGTGTATGACGCAAAATTTGGCGGTGCAGAAATGTT 240
QY 241 gttaaacagaacactcaagaacattcgttaattgattgctcggttttcaactttggc 300
|||||
Db 241 GTTAAACAGAAACTCAGCAAACTTCGTAATGATGCTCGTTTATCACTTTTGGC 300
QY 301 atctatactcgcctggaagcccggtatattgctcacaaatgcttgcacatgataatg 360
|||||
Db 301 ATCTATACTCCGCTGGAAGCCCGGGTATATGCTCACAATAGTTGCCCATATGATGGG 360
QY 361 agctatctcgcgaattcc 378
|||||
Db 361 AGCTCATCTGCGAATTC 378

RESULT 3

US-09-023-221A-1
Sequence 1, Application US/09023221A
Patent No. 6087128

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: ROBINSON, SHELEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.221A
FILING DATE: 12-FEB-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-023-221A-1

	Query Match	89.9%	Score 339.8	DB 3	Length 760	
	Best Local Similarity	98.0%	Pred. No. 8.1e-100			
	Matches 344	Conservative	0	Mismatches 7	Indels	Gaps
QY	21	gccccgagatcatcagcgcgagatcaataagaatgaanaaaatgctatttttcgcgcctcgcg	80			
Db	279	gccccgttttaaacatgcacgagatattatgaatgaaaaaaatgtratttttcgcgcgcctcgcg	338			
QY	81	aatgctatttacagaatgctcacaacaaagttactgtgtggaacaaacgcagacag	140			
Db	339	aatgcgtttttacagagatgtgcctcaacaaacggtttactgttggaacaaacgcacagcact	398			
QY	141	aacgcacaaagaaacccatcactcatcatcttcttgcttcggaattggcacaagagaaac	200			
Db	399	aacacacaaagaaacccatcactcatcattcttcttcggaattggcacaagagaaac	458			
QY	201	tgctgatcagcacaacattgtgcgcgtgcgaaaaatgtgttaaaaacgaaactcagca	260			
Db	459	tgttcattcagcagcaaaattttgtcggcggtgcacaaaattgtgttaaaacgaatctcagca	518			
QY	261	aacattcgtaaatgagattgtctcgttttatacactttgycatctactcgcctggaagc	320			
Db	519	aacattcgtaaatgagattgtctcgttttatacacttttgcatctattccctcggaagc	578			
QY	321	ccgggtatattgctcacaaatgttgcacatcgatatgtgggaactcatctgc	371			
Db	579	ccgggtatattgctcacaaatgttgcacatcagatattggggaactcatctatctgc	629			

RESULT 4
 US-09-282-352A-1
 : Sequence 1, Application US/09282352A
 Patent No. 6187321
 GENERAL INFORMATION:
 APPLICANT: NOLAN, LISA K.
 APPLICANT: HORNE, SHELLEY M.
 APPLICANT: ROBINSON, MICHAEL
 TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.
 STREET: 119 NORTH FOURTH STREET, SUITE 203
 CITY: MINNEAPOLIS
 STATE: MN
 COUNTRY: U.S.A.
 ZIP: 55401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/282.352A
 FILING DATE: 31-MAR-1999
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/023.221
 FILING DATE: 12-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: SANBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41.287
 REFERENCE/DOCKET NUMBER: 255.00010102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1226
 TELEFAX: (612) 305-1228
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 760 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-282-352A-1

Query Match	89.9%	Score 339.8	DB 4	Length 760
Best Local Similarity	98.0%	Pred. No. 8.1e-100		
Matches 344	Conservative 0	Mismatches 7	Indels 0	Gaps 0
Qy	21	gccccggtatccatgcagcagataaagaatgaaaaaagtattattcttcgcgcgtcgtgc	80	
Db	279	gccccgtttttAACATGACGAGATATATAGATGAAAAAATGTTATTTTCGCCGCTGTGC	338	
Qy	81	aatgcttatccaggaatgctcacaacaacglttaactgltggaacaaacgcagacagt	140	
Db	339	AATGCTTATTCACAGATGTGCTCAACAAACGTTTACTGTTGGAAACAAACGACAGCAGT	398	
Qy	141	aacacccaaagaaacaccatccatcatcatcttcttglttcggaatttgacaagagaaaaac	200	
Db	399	AACACCAAAAGGAAMACCATCATCAGATCAATTTCTTCGTTTCGGAAATGGCAAGAGAAAAAC	458	
Qy	201	tgttgatgcagcccaaatcttgctgcgctgcagaaaatgtgttaaacagaacccagca	260	
Db	459	TGTTGATGCACGCCAAATTTGTGGCGGTGCAGAAAATGTGTTAAACGAAACTCACGA	518	
Qy	261	aacatcgtlaaatggaattgctcgtgttatacaactlltggacataactacgcgtggaac	320	
Db	519	AACATTCCTAAATGATGTGCTGCGTTTATCATCTTTGGACATCTPATCTCCGCTGAAGC	578	
Qy	321	ccgggtatattgctcacaaatagttgccatcgatattggggagctaatctgc	371	
Db	579	CCGGGTATATTGCTCACAAATAGTTCGCCATCATATGGGAGCTCATATCTGC	629	

RESULT 5
 US-09-023-221A-22
 Sequence 22, Application US/09023221A
 Patent No. 6087128
 GENERAL INFORMATION:
 APPLICANT: NOLAN, LISA K.
 APPLICANT: HORNE, SHELLEY M.
 TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: MOETING, RAASCH & GEBHARDT P.A.
 STREET: 119 NORTH FOURTH STREET, SUITE 203
 CITY: MINNEAPOLIS
 STATE: MN
 COUNTRY: U.S.A.
 ZIP: 55401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,221A
 FILING DATE: 12-FEB-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: SANDBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41,287
 REFERENCE/DOCKET NUMBER: 235.00010101
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1226
 TELEFAX: (612) 305-1228
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-023-221A-22

Query Match 81.7%; Score 309; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.2e-90;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 34 atgcagataaataagatgataaaatgtatatttctgcgcctctggcaatgtattaca 93
DB 1 ATGCAGATAAATAAGATGATAAAATGTTATTTCGGCGCTGGCAATGCTTATTACA 60
OY 94 ggaatgtctcaacaacgcttactgttggaaacacgcagcagtaacaccaaaggaa 153
DB 61 GGATGTGCTCAACAACGCTTACTGTGGAAACCAACGACGACTAACACCAAGGAA 120
OY 154 accatcactcatcattcttctgttcgggaattggacaagaagaacatgtatgcagcc 213
DB 121 ACCATCACCATCATCTTCTGCTTGGGAATGGACAGAGAAAACCTTTGATCAGCC 180
OY 214 aaattgtgctgcagtgacagaataatgtttaaacaagaactcagcaaacattcgtaaat 273
DB 181 AAAATTGTGGCGGTGCAGAAAATGTTTAAACAGAACTCAGCAAACTTCGTAAT 240
OY 274 ggaatgtctggtttatacaacttggcactatcactcgcgtggaagccgggtatattgc 333
DB 241 GGATGTGCTGCTTATTATCATCTTGGCACTATCTCCGCTGGAAGCCCGGTATATTGC 300
OY 334 tcacaatag 342
DB 301 TCACAATAG 309
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RESULT 6

US-09-282-352A-22
Sequence 22, Application US/09282352A

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-282-352A-22

Query Match 81.7%; Score 309; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.2e-90;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 34 atgcagataaataagatgataaaatgtatatttctgcgcctctggcaatgtattaca 93
DB 1 ATGCAGATAAATAAGATGATAAAATGTTATTTCGGCGCTGGCAATGCTTATTACA 60
OY 94 ggaatgtctcaacaacgcttactgttggaaacacgcagcagtaacaccaaaggaa 153
DB 61 GGATGTGCTCAACAACGCTTACTGTGGAAACCAACGACGACTAACACCAAGGAA 120
OY 154 accatcactcatcattcttctgttcgggaattggacaagaagaacatgtatgcagcc 213
DB 121 ACCATCACCATCATCTTCTGCTTGGGAATGGACAGAGAAAACCTTTGATCAGCC 180
OY 214 aaattgtgctgcagtgacagaataatgtttaaacaagaactcagcaaacattcgtaaat 273
DB 181 AAAATTGTGGCGGTGCAGAAAATGTTTAAACAGAACTCAGCAAACTTCGTAAT 240
OY 274 ggaatgtctggtttatacaacttggcactatcactcgcgtggaagccgggtatattgc 333
DB 241 GGATGTGCTGCTTATTATCATCTTGGCACTATCTCCGCTGGAAGCCCGGTATATTGC 300
OY 334 tcacaatag 342
DB 301 TCACAATAG 309
```

RESULT 7

US-09-023-221A-5
Sequence 5, Application US/09023221A

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-023-221A-5

Query Match 72.3%; Score 273.2; DB 3; Length 309;
Best Local Similarity 96.8%; Pred. No. 1.3e-78;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 34 atgcagataataagaatgaataaataatgtattcttcgcgcgtctgcaatgtattaca 93
1 ATGCAGATTAATAAGATGAATAAATGTTATTTCTGCCCCCTCGCAATGCTATTACA 60
DB 94 ggaatgtctcaacaacggttactgttgaacaacaacgacagcaagtaacacaaaggaa 153
61 GGATGTCTCTCAACAACGTTTACTGTTGGAACAACCGACAGTAACACCAAGAA 120
QY 154 accatcactatcatcttcttcgttgcggaattggaacaagaagaactgttgcagcc 213
121 ACCATCACTCATCTCTTCTGTTCCCAATTGAC-AGAGAAACTGTTGATGCAGCC 179
DB 214 aaatttg-tggcggtgcagaaatgttgttaaaacagaacactcagcaacatcgtaa 272
180 AAATTGTGGGGGGGAGAAAATGTTTAAACAGAAACTCAGCAATTCGTAA 239
QY 273 tggattgctcggttttatacactttggcatcactacgcgtggaagccgggtatattg 332
240 TGCATTCGCCGCTTTATCACTTTTGGCATCTATACCTCCGGGAAACCGGTGATATG 299
DB 333 ctcaaatag 342
300 CTCACAATAG 309

RESULT 8

US-09-282-352A-5
Sequence 5, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELEY M.

APPLICANT: ROBINSON, MICHAEL

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,352A

FILING DATE: 31-MAR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/023,221

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,00010102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-282-352A-5

Query Match 72.3%; Score 273.2; DB 4; Length 309;
Best Local Similarity 96.8%; Pred. No. 1.3e-78;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 34 atgcagataataagaatgaataaataatgtattcttcgcgcgtctgcaatgtattaca 93
1 ATGCAGATTAATAAGATGAATAAATGTTATTTCTGCCCCCTCGCAATGCTATTACA 60
DB 94 ggaatgtctcaacaacggttactgttgaacaacaacgacagcaagtaacacaaaggaa 153
61 GGATGTCTCTCAACAACGTTTACTGTTGGAACAACCGACAGTAACACCAAGAA 120
QY 154 accatcactatcatcttcttcgttgcggaattggaacaagaagaactgttgcagcc 213
121 ACCATCACTCATCTCTTCTGTTCCCAATTGAC-AGAGAAACTGTTGATGCAGCC 179
DB 214 aaatttg-tggcggtgcagaaatgttgttaaaacagaacactcagcaacatcgtaa 272
180 AAATTGTGGGGGGGAGAAAATGTTTAAACAGAAACTCAGCAATTCGTAA 239
QY 273 tggattgctcggttttatacactttggcatcactacgcgtggaagccgggtatattg 332
240 TGCATTCGCCGCTTTATCACTTTTGGCATCTATACCTCCGGGAAACCGGTGATATG 299
DB 333 ctcaaatag 342
300 CTCACAATAG 309

RESULT 9

US-09-470-618-13
Sequence 13, Application US/09470618
Patent No. 6200560

GENERAL INFORMATION:

APPLICANT: Couto, Linda B.

APPLICANT: Colosi, Peter C.

TITLE OF INVENTION: Yarn-associated Vectors for Expression of Factor VIII

FILE REFERENCE: Avigen-04082

CURRENT APPLICATION NUMBER: US/09/470,618

CURRENT FILING DATE: 1999-12-22

EARLIER APPLICATION NUMBER: 09/364,862

EARLIER FILING DATE: 1999-07-30

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER FILING DATE: 1999-03-24

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 11933

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-470-618-13

Query Match 67.8%; Score 256.4; DB 4; Length 11933;
Best Local Similarity 88.5%; Pred. No. 1.7e-72;
Matches 278; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 33 catgcagataataagaatgaataaataatgtattcttcgcgcgtctgcaatgtattaca 92
9294 catgcagataataagaatgaataaataatgtattcttcgcgcgtctgcaatgtattaca 9353
DB 93 aggatgtctcaacaacggttactgttgaacaacaacgacagcaagtaacacaaaggaa 152
9354 aggatgtctcaacaacggttactgttgaacaacaacgacagcaagtaacacaaaggaa 9413
QY 153 aaccatcactatcatcttcttcgttgcggaattggaacaagaagaactgttgcagc 212

Db 9414 aaccatccaccatcattcttcgttcgtggaattgagcagaagaatacgttcgacgc 9473
Oy 213 caaaattgtgctgagagaataatgtgttaaacagaaactcgcgaacattcgtaa 272
Db 9474 caaaattgtgctgagagaataatgtgttaaacagaaactcgcgaacattcgtaa 9533
Oy 273 tggattgctggtttatcacttttgcatctatactcgcgtggaagccgggtatattg 332
Db 9534 tggattgctggtttatcacttttgcatctatactcgcgtggaagccgggtatattg 9593
Oy 333 ctcaacaatgtgc 346
Db 9594 ctcaacaatgtgc 9607

US-09-364-862-13
Sequence 13, Application US/09364862
Patent No. 6221349
GENERAL INFORMATION:
APPLICANT: Couto, Linda B.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
FILE REFERENCE: AVIGEN-03743
CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 13
LENGTH: 11933
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-364-862-13

Query Match 67.8%; Score 256.4; DB 4; Length 11933;
Best Local Similarity 88.5%; Pred. No. 1.7e-72;
Matches 278; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Oy 33 catcagagataataagatgaaaaaattgttattcttcgcgcctctgcaatgttattac 92
Db 9294 catcagagataataagatgaaaaaattgttattcttcgcgcctctgcaatgttattac 9353
Oy 93 aggtgtgctcaacaagaagtttactgttggaacaacacgcagacgaatgaacccaaga 152
Db 9354 aggtgtgctcaacaagaagtttactgttggaacaacacgcagacgaatgaacccaaga 9413
Oy 153 aaccatccatcattcttcgttcgttggaattggaacaagaagaactgttgatgcagc 212
Db 9414 aaccatccatcattcttcgttcgttggaattggaacaagaagaactgttgatgcagc 9473
Oy 213 caaaattgtgctgagagaataatgtgttaaacagaaactcgcgaacattcgtaa 272
Db 9474 caaaattgtgctgagagaataatgtgttaaacagaaactcgcgaacattcgtaa 9533
Oy 273 tggattgctggtttatcacttttgcatctatactcgcgtggaagccgggtatattg 332
Db 9534 tggattgctggtttatcacttttgcatctatactcgcgtggaagccgggtatattg 9593
Oy 333 ctcaacaatgtgc 346
Db 9594 ctcaacaatgtgc 9607

RESULT 11
US-09-023-221A-6
Sequence 6, Application US/09023221A
Patent No. 6087128
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-6

Query Match 66.7%; Score 252; DB 3; Length 309;
Best Local Similarity 88.6%; Pred. No. 8.4e-72;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Oy 34 atcagagataataagatgaaaaaattgttattcttcgcgcctctgcaatgttattac 93
Db 1 ATCGGGAATACACCATGAAAAAATGCTACTGCTACTGCGCTGCGCTGCTTAATACA 60
Oy 94 ggaatgtctcaacaagcttactgttggaacaacacgcagacgaatgaacccaaga 153
Db 61 GGATGTGCTCAACAGACGTTACTGTCAAAACAAACCGGCGAGTAGACCAACAAAGAA 120
Oy 154 accatccatcattcttcgttcgttggaattggaacaagaagaagaactgttgatgcagc 213
Db 121 ACCATCCACCAACATTTCTTCCTTCTGGAATGGGAGAAAGAAACGTCATCCACGC 180
Oy 214 aaattgtgctgagagaataatgtgttaaacagaaactcgcgaacattcgtaa 273
Db 181 AAAATTGTGCGGCGGCGCAAAAATGTGTAAACAGAAACCCACCAAACTCTAAT 240
Oy 274 ggaatgtcgtttatcacttttgcatctatactcgcgtggaagccgggtatattg 333
Db 241 GGATGTGCTGAGTTTATTAATTAGGCAATTAATCTCCGCTGGAAGCGGTGTATTGC 300
Oy 334 tcacaata 341
Db 301 TCACAATA 308

RESULT 12
US-09-282-352A-6

Query Match	66.7%	Score 252	DB 4	Length 309	
Best Local Similarity	88.6%	Pred. No. 8.4e-72			
Matches 273	Conservative 0	Mismatches 35	Indels 0	Gaps 0	

OY	34	a t g c g a t a a t a a g a t g a a a a a a a t g t a t t t c t g c g c t c t g y c a a t g t t a t c a	93
Db	1	A Y C G G A N T A A C A C C A T G A A A A A A A A T G C T A C T G C G T A C G C C T G C C C T G T T A T T C A	60
OY	94	g g a t g t g t c t c a a a a a g c t t t a c t c t g t t g g a a a c a a c g c a g c g c g t a c c a a a g g a a	153
Db	61	G G A T T G C T C A A C A C A C G T T A C T T T A A A A C C A A C C G C A G C A G T A C C A C C A A A G G A A	120
OY	154	a c c a t c a c t a c t a c t a t t c t g t t c g g a a t t g g a a c a a g a a a a c t g t a t c a g c	213
Db	121	A C C A T C A C C C A T C A T T T C T C G T T C T G A A T T G G C G A G A A A A A C T G C A T C A G C	180
OY	214	a a a a t t g t g c g y t g c a g a a a t g t g t t a a a c a g a a a c t c a g c a a a c t t g t a a t	273
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OY	274	g g a t t g c t c g g t t t a t a c t a c t t t g g c a t c t a c t c g c t g y a a g c c g g t a t a t g c	333
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OY	334	t c a c a a t a 341	
Db	301	T C A C A T A 308	

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Query Match          9.0%: Score 34.2; DB 4; Length 1519;
Best Local Similarity 67.6%: Pred. No. 0.15; 23; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 0;

QY      186  tgcacagagaagaactcttgatgcagccaaatattgtgcgctgcagaaacttgcttaa 245
          ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       992  TGGCAAAAGAGATACAGATGAAACAAAGATTGTGCCATACAGAAATAGCTTCG 1051

QY      246  aacaggaactc 256
          || ||||| ||

Db       1052  AAAAGAAATC 1062

RESULT  14
US-08-743-637B-1
; Sequence 1, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND

```

;; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
;; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
;; NUMBER OF SEQUENCES: 273
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: QUARLES & BRADY
;; STREET: 411 EAST WISCONSIN AVENUE
;; CITY: MILWAUKEE
;; STATE: WISCONSIN
;; COUNTRY: USA
;; ZIP: 53202-4497
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,637B
;; FILING DATE: 04-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/526,840
;; FILING DATE: 11-SEP-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BAKER, Jean C.
;; REGISTRATION NUMBER: 35,433
;; REFERENCE/DOCKET NUMBER: 850586,90012
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (414) 277-5000
;; TELEFAX: (414) 277-5591
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1817 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Enterococcus faecalis
;; US-08-743-637B-1

Query Match 8.9%; Score 33.6; DB 2; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.25;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

OY 160 accatcattcttcgttcggaattgagcaagaagaacgttgatcgagccaaatt 219
DB 1211 ACCTATGCTTCCTTGAATGATGAGTTGGTCATGAATGACATGCTGAGGAACT 1270
OY 220 tctgagcggtgcagaaatgttgttaaacagaaactcagcaaacattcgtaattgattg 279
DB 1271 ACTGCGGCTTAAATATTAGACAAATCAGTGCCTTGAAATGAATCTATTCTGATTG 1330
OY 280 ctgcgtttatcacttttgcatctactcc 311
DB 1331 ATGGGTATATATTTCGGGTGATCTAATCC 1362

RESULT 15
US-08-526-840B-1
; Sequence 1, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: QUARLES & BRADY

;; STREET: 411 East Wisconsin Avenue
;; CITY: Milwaukee
;; STATE: Wisconsin
;; COUNTRY: USA
;; ZIP: 53202-4497
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/526,840B
;; FILING DATE: 11-SEP-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/304,732
;; FILING DATE: 12-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BAKER, Jean C.
;; REGISTRATION NUMBER: 35,433
;; REFERENCE/DOCKET NUMBER: 850586,90012
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (414) 277-5000
;; TELEFAX: (414) 277-5591
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1817 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Enterococcus faecalis
;; US-08-526-840B-1

Query Match 8.9%; Score 33.6; DB 3; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.25;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

OY 160 accatcattcttcgttcggaattgagcaagaagaacgttgatcgagccaaatt 219
DB 1211 ACCTATGCTTCCTTGAATGATGAGTTGGTCATGAATGACATGCTGAGGAACT 1270
OY 220 tctgagcggtgcagaaatgttgttaaacagaaactcagcaaacattcgtaattgattg 279
DB 1271 ACTGCGGCTTAAATATTAGACAAATCAGTGCCTTGAAATGAATCTATTCTGATTG 1330
OY 280 ctgcgtttatcacttttgcatctactcc 311
DB 1331 ATGGGTATATATTTCGGGTGATCTAATCC 1362

Search completed: July 23, 2002, 13:45:07
Job time: 5108 sec

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